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OM protein - protein search, using sw model
Run on: June 3, 2004, 08:53:00 ; Search time 17 Seconds
(without alignments)
744.297 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMDKYSGKACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues 141681
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1287	100.0	281	1 TN10_HUMAN	P50591 homo sapien
2	863	67.1	291	1 TN10_MOUSE	P50592 mus musculus
3	250.5	19.5	318	1 TN11_RAT	Q95922 r tumor nec
4	238.5	18.5	316	1 TN11_MOUSE	Q35235 m tumor nec
5	235.5	18.3	317	1 TN11_HUMAN	O14788 h tumor nec
6	189.5	14.7	279	1 TNF6_MOUSE	P41047 mus musculus
7	185.5	14.4	280	1 TNF6_CERTO	Q9bdn1 cercopithec
8	183.5	14.3	280	1 TNF6_MACMU	Q9my16 macaca mula
9	182.5	14.2	281	1 TNF6_HUMAN	P48023 homo sapien
10	182	14.1	282	1 TNF6_PIG	Q9bea8 sus scrofa
11	177.5	13.8	278	1 TNF6_RAT	P36940 rattus norv
12	171	13.3	272	1 TNF5_CHICK	Q9i8d8 gallus gall
13	160	12.4	174	1 TN15_HUMAN	O95150 homo sapien
14	159.5	12.4	240	1 TN14_MOUSE	O43557 homo sapien
15	152.5	11.8	239	1 TN14_MOUSE	Q9gyh9 mus musculus
16	152	11.8	261	1 TNF5_BOVIN	P51749 bos taurus
17	140	10.9	261	1 TNF5_AOTTR	Q9bdm3 actus trivi
18	140	10.9	261	1 TNF5_CALJA	Q9bdm3 callithrix
19	137.5	10.7	260	1 TNF5_MOUSE	P27548 mus musculus
20	137	10.6	261	1 TNF5_HUMAN	P29965 homo sapien
21	137	10.6	261	1 TNF5_MACMU	Q9bdc7 macaca mula
22	136.5	10.6	261	1 TNF5_RABIT	P04924 cryptolagus
23	136.5	10.6	260	1 TNF5_FELCA	Q97605 felis silve
24	134.5	10.5	204	1 TNF5_PIG	P26445 sus scrofa
25	134.5	10.5	204	1 TNF5_CANFA	Q97626 canis fami
26	132.5	10.3	234	1 TNF5_CAVPO	P51435 cavia porce
27	132	10.3	261	1 TNF5_PIG	Q95mg5 sus scrofa
28	131.5	10.2	260	1 TNF5_RAT	Q92272 rattus norv
29	130	10.1	232	1 TNF4_PIG	P23563 sus scrofa
30	129.5	10.1	235	1 TNF5_PERLE	Q96939 peromyscus
31	127.5	9.9	204	1 TNF6_BOVIN	Q06600 bos taurus
32	126	9.8	234	1 TNF4_HORSE	P29553 equus cabal
33	125.5	9.8	253	1 TNF4_SPAU	Q9jfg3 sparus aura

ALIGNMENTS

RESULT 1

ID	TN10_HUMAN	STANDARD;	PRT;	281 AA.
AC	P50591	1996 (Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).			
GN	TNFSF10 OR TRAIL OR APO2L			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=96111955; PubMed=877713;			
EX	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,			
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,			
RA	Goodwin R.G.,			
RT	"Identification and characterization of a new member of the TNF			
RT	family that induces apoptosis."			
RL	Immunity 3:673-682(1995).			
[2]	SEQUENCE FROM N.A.			
RP	TISSUE=Placenta;			
EX	MEDLINE=96278649; PubMed=8663110;			
RA	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,			
RA	Ashkenazi A.,			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor			
RT	necrosis factor cytokine family."			
RL	J. Biol. Chem. 271:12687-12690(1996).			
[3]	SEQUENCE FROM N.A.			
RP	TISSUE=Lymph;			
EX	MEDLINE=12477932; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richardson S., McEwan P.J., McKernan K.J., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting R.W., Young A.C., Shevchenko Y., Scuffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

[4]
 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 MEDLINE=20017054; PubMed=10549288;
 Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 Kelley R.F., Ashkenazi A., de Vos A.M.;
 "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 complex with death receptor 5.";
 Mol. Cell 4:563-571(1999).
 [5]
 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 PubMed=10542098;
 Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 Jones E.Y., Screaton G.R.;
 "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 specificity in apoptotic initiation.";
 Nat. Struct. Biol. 6:1048-1053(1999).
 [6]
 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 MEDLINE=99413670; PubMed=10485660;
 Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 Sung Y.C., Oh B.-H.;
 "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 selective antitumor activity.";
 Immunity 11:253-261(1999).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 may be modulated by binding to the decoy receptors
 TNFRSF10C/TRAILR3, TNFRSF10B/TRAILR4 and TNFRSF11B/OPG that cannot
 induce apoptosis.
 CC -1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 trimer.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 AND PROSTATE.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 EMBL; U37518; AAC50332.1; -;
 EMBL; U57059; AAB01233.1; -;
 EMBL; BC032722; AAH32722.1; -;
 PDB; 1DQ3; 22-OCT-99.
 PDB; 1D4V; 01-NOV-99.
 PDB; 1D2Q; 11-FEB-00.
 PDB; 1DG6; 26-SEP-01.
 Genew; HGNC:11925; TNFRSF10.
 MIM; 603598; -;
 GO; GO:0005887; C:integral to plasma membrane; TAS.
 GO; GO:0005825; C:soluble fraction; TAS.
 GO; GO:0005825; F:receptor binding; TAS.
 GO; GO:0005825; F:receptor binding; TAS.
 GO; GO:0007267; P:cell-cell signaling; TAS.
 GO; GO:0006917; P:induction of apoptosis; TAS.
 GO; GO:0007165; P:signal transduction; TAS.
 InterPro; IPR006052; TNF family.
 InterPro; IPR008983; TNF-like.
 InterPro; IPR003636; TNF_subf.
 Pfam; PF00229; TNF_1.
 ProDom; PD002012; TNF_subf; 1.
 SMART; SM00207; TNF; 1.
 PROSITE; PS00251; TNF_1; 1.
 PROSITE; PS00049; TNF_2; 1.
 Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 Zinc; 3D-structure.
 DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 39 281
 FT METAL 230
 FT STRAND 127
 FT TURN 130
 FT TURN 131
 FT TURN 137
 FT STRAND 139
 FT STRAND 149
 FT STRAND 150
 FT STRAND 163
 FT STRAND 165
 FT TURN 170
 FT TURN 171
 FT STRAND 172
 FT STRAND 173
 FT STRAND 180
 FT STRAND 205
 FT STRAND 213
 FT STRAND 220
 FT STRAND 237
 FT TURN 250
 FT TURN 252
 FT STRAND 253
 FT STRAND 260
 FT HELIX 263
 FT STRAND 265
 FT TURN 266
 FT TURN 270
 FT STRAND 272
 FT TURN 274
 FT TURN 281
 SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;
 Query Match 100.0%; Score 1287; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 8.3e-99;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQMLRTSEE 60
 DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQMLRTSEE 98
 QY 61 TISTVQEKQNISPLVREGRGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNISPLVREGRGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHNLNGELVHEKGFYIYSQTYFRFQBEIKENTKDKQKQVYIYKTSYPD 180
 DB 159 SGHSFLSNLHNLNGELVHEKGFYIYSQTYFRFQBEIKENTKDKQKQVYIYKTSYPD 218
 QY 181 PILLMKARNCSKDAEYGLYSTYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKARNCSKDAEYGLYSTYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281
 RESULT 2
 ID TN10 MOUSE STANDARD; PRT; 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 RT family that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

Query Match 19.5%; Score 250.5; DB 1; Length 318;
Best local Similarity 28.5%; Pred. No. 1.9e-13;
Matches 75; Conservative 46; Mismatches 87; Indels 55; Gaps 10;

QY 9 DKYSKSGIACF-----LKED-----DSVWDNDESMNSCWQVQWQOLRVKMLRTSE 59
DB 78 NRSEOSTRCFYILRLRENTGLQDSETEALPDSCRRNKQAFQ----- 125
QY 60 ETISTVQEKQONISPLVRERGPOR---VAAHITGT-----RGRS-----NTLSS 100
DB 126 --GAVQRELQHLV-----GPQRFSGVPAMMGSLDVARRGKPEAQFAHLITNAADI 176
QY 101 PMSKNEKALGRKINSHESSGHSFSLNHLRNGELVIEHKGPYIYISOTYFRFQBEIKE 160
DB 177 PGGSHKVSLS-----SSWYHDA--GKAKISNMTLSLKLVRVQDGFYIYANICFRHHETS 231
QY 161 NTXNDKQWQYIYKYT--SYDPDILLKMSARNSCKSKDAEYGLYSIVQGGIFELKENDRIF 219
DB 232 VPADYQLQWVYVVKTSIKIPSSHNLMKGGSTKWSGNSFHFYSINVGGFFKLAGEEIS 291
QY 220 VSVTNEHLIDMDEASFPFGLV 242
DB 292 VQVSNPSSLDPDQDQATYFGAKV 314

RESULT 4

TN11_MOUSE STANDARD; PRT; 316 AA.

AC Q35235; Q35306; Q9JUK8; Q9JUK9; Q9RIY0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
(OCIF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RN RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hybridoma;
RX MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Arton J., Robinson E., Orlick J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.,
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [2]
RN RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thymic lymphoma;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [3]
RN RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow;
RX MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast

RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [4]
RN RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow stroma;
RX MEDLINE=9818248; PubMed=9520411;
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M., Tada E.,
RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tada E.,
RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT "Osteoclast differentiation factor is a ligand for
RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT to TRANCE/RANKL.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN [5]
RN RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=129;
RX MEDLINE=99214075; PubMed=10196481;
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA Ueda M., Higashio K.;
RT "Cloning and characterization of the gene encoding mouse osteoclast
RT differentiation factor.";
RL Gene 230:121-127(1999).
RN [6]
RN RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21150053; PubMed=11250921;
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT "Determination of three isoforms of the receptor activator of nuclear
RT factor-kappaB ligand and their differential expression in bone and
RT thymus.";
RL Endocrinology 142:1419-1426(2001).
RN [7]
RN RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX MEDLINE=99240759; PubMed=10224132;
RA Lum L., Wong B.R., Josten R., Becherer J.D., Erdjument-Bromage H.,
RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
RT "Evidence for a role of a tumor necrosis factor-alpha
RT (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, a
RT TNF family member involved in osteoclastogenesis and dendritic cell
RT survival.";
RL J. Biol. Chem. 274:13613-13618(1999).
RN [8]
RN RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX MEDLINE=21464816; PubMed=11581298;
RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
RT of receptor-ligand specificity.";
RL J. Clin. Invest. 108:971-979(2001).
RN [9]
RN RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RX MEDLINE=21839021; PubMed=11733492;
RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
RT "Crystal structure of the extracellular domain of mouse RANK ligand at
RT 2.2-A resolution.";
RL J. Biol. Chem. 277:6631-6636(2002).
RN [10]
RN RP FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcaemia of malignancy.
CC SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC (isoforms 1 and 2); Cytoplasmic (isoform 3).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=O35235-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O35235-2; Sequence=VSP_006449;
CC Name=3;
CC IsoId=O35235-3; Sequence=VSP_006448;

CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE TRABECULAR BONE AND LUNG.

CC -!- PTM: N-glycosylated.

CC -!- PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.

CC -!- DISEASE: Deficiency in TNFSF11 results in failure to form lobulo-alveolar mammary structures during pregnancy, resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, including the limbs, skull, and vertebrae and have marked chondrodysplasia, with thick irregular growth plates and a relative increase in hypertrophic chondrocytes.

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC -----

CC EMBL; AF013170; AAC71061.1; -

CC EMBL; AF019048; AAB86812.1; -

CC EMBL; AF053713; AAC40113.1; -

CC EMBL; AB008426; BAA25425.1; -

CC EMBL; AB022039; BAA36970.1; -

CC EMBL; AB022036; BAA36970.1; JOINED.

CC EMBL; AB022037; BAA36970.1; JOINED.

CC EMBL; AB022038; BAA36970.1; JOINED.

CC EMBL; AB032771; BAA97257.1; -

CC EMBL; AB032772; BAA97258.1; -

CC EMBL; AB036798; BAA97259.1; -

CC PDB; 1J7Z; 28-JAN-03.

CC PDB; 1IQA; 14-JAN-03.

CC MGI; 1100089; Tnfsf11.

CC GO; GO:0009887; P:organogenesis; IMP.

CC GO; GO:0001503; P:cell differentiation; IMP.

CC InterPro; IPR006052; TNF family.

CC InterPro; IPR008983; TNF-like.

CC InterPro; IPR003636; TNF subf.

CC Pfam; PF00229; TNF; 1.

CC ProDom; PD002012; TNF subf; 1.

CC SMART; SM00207; TNF; 1.

CC PROSITE; PS00251; TNF 1; FALSE_NEG.

CC PROSITE; PS00049; TNF 2; 1.

CC Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane; Signal-anchor; 3D-structure; Alternative splicing.

CC CHAIN 1 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, MEMBRANE FORM.

CC CHAIN 139 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM.

CC DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

CC DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).

CC SITE 138 139 CLEAVAGE.

CC CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC VARSPIC 1 117 Missing (in isoform 3).

CC VARSPIC 14 44 (FTId=VSP_006448).

CC SSMGSPGVPEHGFHPAPAPAPAPPA -> TP (in isoform 2).

CC (FTId=VSP_006449).

CC G -> D (IN REF. 2).

CC MISSING (IN REF. 5).

CC CONFLICT 99 99

CC CONFLICT 141 143

CC STRAND 164 169

CC TURN 171 172

CC STRAND 181 182

FT STRAND 186 187

FT TURN 191 192

FT STRAND 194 196

FT STRAND 198 201

FT TURN 202 203

FT STRAND 204 207

FT STRAND 211 224

FT HELIX 225 227

FT STRAND 234 245

Query Match 18.5%; Score 238.5; DB 1; Length 316;

Best Local Similarity 27.4%; Pred. No. 1.9e-12;

Matches 71; Conservative 44; Mismatches 95; Indels 49; Gaps 9;

Qy 9 DKYSKSGIACF-----LKEDDSYWDP--NDEESMSPCMQVKQLQVLEKMLRTSEET 61

Db 78 NRISDSTHCFYRILRLHENAGLQDSTLESEDLPSCRMKQAFQGVQK----- 128

Qy 62 ISTVQEQQNISPL-----VREGPQVRA--AHITGTRGSNTLSPNSK 104

Db 129 -----ELQHIVGQRFPSGAPAMMEGSLDVAQRKPEAQPFALHT-----INAASIPSGS 178

Qy 105 NEKALGRKINSWSSRGSHSFLNLHLENGELVIHEKGFYIYSQTYERFQEBIKENTKN 164

Db 179 HKVTL-----SSVHDDR--GWAKISNMTLSNGKLRVQDGFYLYANICFRHHETSGSVPTD 233

Qy 165 DKQWVQYIYKYT--SYDPILLMKSARNSCWSKDAETGLYSIYQGGIFELKENDRIFVSVT 223

Db 234 YLQLMVTVVVTKTSIKIPSSHNLKMGSTKQWNSGSEFHYGINVGGPFKLAGEISIQVS 293

Qy 224 NEHLIDMDHEASFGAFLV 242

Db 294 NPSLLDPDQDATVFGAFKV 312

RESULT 5

TN11_HUMAN STANDARD; PRT; 317 AA.

ID TN11_HUMAN

AC O14788; O14723; Q96Q17; Q9P2Q3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).

DE Differentiation factor (ODF).

GN TNFSF11 OR RANKL OR TRANCE OR OPGL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_taxid=9606;

RN [1]_taxid=9606;

SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Bone marrow, and Peripheral blood;

RX MEDLINE=98032977; PubMed=9367155;

RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tonetsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D., Galibert L.

RA "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function."

RL Nature 390:175-179(1997).

SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Lymph node;

RX MEDLINE=98227661; PubMed=9568710;

RA Lacey D.L., Rimm E., Tan H.-L., Kelley M.J., Dunstan C.R., Hau H., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hau H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.

RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."

RT Cell 93:165-176(1998).

[3]
 RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA Ikeda T., Kuroyama H., Hirokawa K.;
 RT "Determination of human RANKL isoforms";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE OF 73-317 FROM N.A.
 RC TISSUE=Thymocytes;
 RX MEDLINE=97460112; PubMed=9312132;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlicki J., Chao M.,
 RA Kalachikov S., Cayani E., Bartlett P.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "RANK is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells";
 RL J. Biol. Chem. 272:25190-25194 (1997).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Tongue;
 RX MEDLINE=20175237; PubMed=10708588;
 RA Nagai M., Kyakumoto S., Sato N.;
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RT encoding a secreted form of ODF/TRANCE that induces osteoclast
 RT formation";
 RL Biochem. Biophys. Res. Commun. 269:532-536 (2000).
 CC -|- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone resorption in humoral
 CC hypercalcemia of malignancy.
 CC -|- SUBUNIT: Homotrimer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O14788-1; Sequence=Displayed;
 CC Name=2; Synonyms=SODF;
 CC IsoId=O14788-2; Sequence=VSP_006447;
 CC Name=3;
 CC IsoId=O14788-3; Sequence=VSP_006446;
 CC -|- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK
 CC IN SLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
 CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
 CC -|- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
 CC -|- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing (By similarity). The cleavage may be
 CC catalyzed by ADAM17.
 CC -|- SIMILARITY: Belongs to the tumor necrosis factor family.

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 CC or send an email to license@sib-sib.ch.

 CC EMBL; AF019047; AAB86811.1; -
 CC EMBL; AF053712; AAC39731.1; -
 CC EMBL; AB064269; BAB79694.1; -
 CC EMBL; AB061227; BAB71768.1; -
 CC EMBL; AB064270; BAB79695.1; -
 CC EMBL; AF013171; AAC51762.1; -
 CC EMBL; AB037599; BAA90488.1; -
 CC HSSP; P50591; 1DQG.
 CC Genew; HGNC:11926; TNFSF11.
 CC MIM; 602642; -
 CC GO; GO:0005576; C:extracellular; NAS.
 CC GO; GO:0005887; C:integral to plasma membrane; NAS.

DR GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR GO; GO:0030316; P:osteoclast differentiation; NAS.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SMO0207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 DR PROSITE; PS00049; TNF_2; 1.
 KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
 KW Signal-anchor; Alternative splicing.
 FT CHAIN 1 317
 FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT MEMBER 11; MEMBRANE FORM.
 FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT MEMBER 11; SOLUBLE FORM (BY SIMILARITY).
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT CLEAVAGE (BY SIMILARITY).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT Missing (in isoform 3).
 FT /FTid=VSP_006446.
 FT VARSPLTC 1 73
 FT Missing (in isoform 2).
 FT /FTid=VSP_006447.
 FT CONFLICT 194 194 A -> G (IN REF. 4).
 FT SEQUENCE 317 AA; 35478 MW; 76617646348097F CRC64;
 Query Match 18.3%; Score 235.5; DB 1; Length 317;
 Best Local Similarity 25.3%; Pred. No. 3.3e-12;
 Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;
 QY 9 DKYSKSGIACF-----LKED-----DSYDNDPDESMNSPCWQVKW-----OLQOLVR 51
 DB 77 NRISGDTHCIYRILRLHENDFOPTLESQDTKLIPDSCKRIKQAFQGVAKELQHV 136
 QY 52 KMILRTSEETI-----STVQEQKQNI SPLVREGRQFVAHI TGTGRSNTLSSPNKNE 106
 DB 137 SQHIRAEKAMVDGSLDLAKRSKLEAQP-----AHLT-----INATDIPSGSHK 181
 QY 107 KALGKINSWESSRSGHSFLSNLRLNGELVIHKEGFYLYSOTYFQEEIKENTKNDK 166
 DB 182 VSL-----SSWYHDR-GWAKISNMTFTSGKLIVNQDGFYLYANICFRHHETSGDLATEYL 236
 QY 167 QMWQVIYKYT-SYDPDILLMKSAENSQSKDAEYGLYSIYQGGIFELKENDRIFVSVTNE 225
 DB 237 QLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSFEHFYSINVGFFKLRSGEISIEVSNP 296
 QY 226 HLIDMDHEASFPGLV 242
 DB 297 SLLOPDQDQATYFGAFKV 313
 RESULT 6
 TNF6_MOUSE
 ID TNF6_MOUSE STANDARD; PRT; 279 AA.
 AC P41047; Q61217; Q9RUF2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN TNFSF6 OR FASL OR APT1LG1 OR GLD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId:10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=94185175; PubMed=7511063;


```
QY 165 DKOMQVYIY-KVTSPDPILLMKASR-NSCWSKDAEYGLYSIQGIFELKENDRIFSV 222
DB 202 NQPLAHKVMRSKYPEDVLMEERLNYCTT--QQIWAHSSYLGAVERNLSADHLYVNI 259
QY 223 TNEHLIDMDEASFFGAF 240
DB 260 SOLSLINFESKTFPGLY 277

RESULT 7
TNF6_CERTO
ID TNF6_CERTO STANDARD; PRT; 280 AA.
AC Q9BDJ1.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
CC -!- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC modulates its effects (By similarity).
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF34847; AK37606.1; -.
DR HSPG; P01375; ATSV.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; P01681; FASLIGAND.
DR PRINTS; P01234; TNFECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 6, MEMBRANE FORM.
FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
```

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FT DOMAIN 1 80 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT TRANSMEM 81 101 CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT PRO-RICH.
FT PRO-PRO.
FT POLY-PRO.
FT CLEAVAGE (BY SIMILARITY).
FT SITE 128 129 POTENTIAL.
FT DISULFID 201 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 14.4%; Score 185.5; DB 1; Length 280;
Best Local Similarity 27.4%; Pred. No. 3.7e-08;
Matches 55; Conservative 42; Mismatches 77; Indels 27; Gaps 8;

QY 44 WQLRQLVRKMI-LR--TSEETISTVQEKQNTISPLVRERGPQRVAAHITGTRSNLTSS 100
DB 101 FQLFHLQKELAELESTSQKHTASSLEKQIGHSPPEKKEQRKVAHLTG-----K 151
QY 101 PMSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIEHKGFYIYSQTYFRFOEIKE 160
DB 152 PMSRMPL-----EWEDT-YGIVLLSGVKYKGGVLINETGLYFYISKYVFRGQ---- 199
QY 161 NTKNDKQMVYIY-KVTSPDPILLMKASRNSCWSKDAEYGLYSIQGIFELKENDRIF 219
DB 200 -SCTNPLSHKVMRSKYPQDLVMEGRKMS-YCTTGQWMAHSSYLGAVERNLTSTDHLY 257
QY 220 VSVTNEHLIDMDEASFFGAF 240
DB 258 VVVSLSLVNFERSQTFPGLY 278

RESULT 8
TNF6_MACMU
ID TNF6_MACMU STANDARD; PRT; 280 AA.
AC Q9NYL6; Q9BDM5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
CC [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M. mulatta, M. fascicularis, and M. nemestrina;
RA Kirii Y., Inoue T., Yoshino K.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC modulates its effects (By similarity).
```

```

CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC -----
CC EMBL; AF344856; AAK37539.1; -.
CC EMBL; AB035138; BAA90294.1; -.
CC EMBL; AB035139; BAA90295.1; -.
CC EMBL; AB035140; BAA90296.1; -.
CC HSSP; P01375; 4TSV.
CC InterPro; IPR008084; Fas_ligand.
CC InterPro; IPR006053; TNF_abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01681; FASLIGAND.
CC PRINTS; PR01234; TNFCROSISFT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS0049; TNF_2; 1.
CC Cytokine; apoptosis; Transmembrane; Glycoprotein; signal-anchor.
CC CHAIN 1 280
CC
CC CHAIN 129 280
CC
CC DOMAIN 1 80
CC TRANSMEM 81 101
CC
CC DOMAIN 102 280
CC
CC DOMAIN 4 69
CC DOMAIN 45 64
CC SITE 128 129
CC DISULFID 201 232
CC CARBOHYD 183 183
CC CARBOHYD 249 249
CC CARBOHYD 259 259
CC CONFLICT 60 60
CC S -> P (IN REF.1).
CC SEQUENCE 280 AA; 31367 MW; F0B2B4D61A132EE4 CRC64;
CC
CC Query Match 14.3%; Score 183.5; DB 1; Length 280;
CC Best Local Similarity 27.4%; Pred. No. 5.4e-08;
CC Matches 55; Conservative 42; Mismatches 77; Indels 27; Gaps 8;
CC
CC Qy 44 WQLRQLVKMI-LR-TSETSTVQKQNIPLVREPCQVAAHITCRGSRNLTGS 100
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Db 101 FQFLHQLKLAELRESTSQHTASLEKQIGHPSPPPEKQKQVAHLTG-----K 151
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Qy 101 PNSKNEALGRKINSWESSGSHFSLNLRNGELVIHEKGYIYISQTYFFRQBEIKE 160
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Db 152 PNSRSMPD-----EWEDT-YGIVLLSGVYKXKGLVINETGLYFYVSKYVFRGQ----- 199
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Qy 161 NTRNDKQWQVIY-KYTSYDDPILLMKARNSCWSDAEVGLVSYIOGGIFELKENDRIF 219
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Db 200 -SCTNPLSHKVVYRNRSKYPODLVMEGRKMS-YCTTGQWMAHSSYLGAVFNLTSDADHLY 257
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Qy 220 VSVTNEHLIDMDHEASFFGAF 240
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Db 258 VNVSELSLVNFEESQTFGLY 278
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC RESULT 9

```

```

TNF6_HUMAN
ID TNF6_HUMAN STANDARD; PRT; 281 AA.
AC P48023; Q952P9;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (Apoptosis antigen ligand) (APIL) (CD178 antigen).
GN TNFSP6 OR FASL OR APILIG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
J. Exp. Med. 181:71-77(1995).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95127560; PubMed=7825947;
RA Takahashi T., Tanaka M., Inatawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
specificity."
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
SEQUENCE FROM N.A. (ISOFORM 1).
RA Schaezel C.E., Poehlmann R., Philippsen P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioaka T., Kasahara A.,
RA Fusamoto H., Kanada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
infection."
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
human Fas ligand that is expressed only in membrane bound form."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RX MEDLINE=97373583; PubMed=9228056;
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
RA Tersikh A., Peitsch M.C., Rechoff J.;
RT "Characterization of Fas (Apo-1, CD95) -Fas ligand interaction.";
RL J. Biol. Chem. 272:18827-18833(1997).
RN [10]
RP PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Itai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RL Nat. Med. 4:31-36(1998)
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects.
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
CC into the extracellular fluid, probably by cleavage form the cell
CC surface.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=PA48023-1; Sequence=Displayed;
CC Name=2;
CC IsoId=PA48023-2; Sequence=VSP_006443, VSP_006444;
CC -!- PTM: N-glycosylated.
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing.
CC -!- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
CC involving hemolytic anemia and thrombocytopenia with massive
CC lymphadenopathy and splenomegaly.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -!- DATABASE: NAME=PRO; NOTE=PROW 2:59-69(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X89102; CAA61474.1; -
DR EMBL; U08137; AAC50071.1; -
DR EMBL; U11821; AAC50124.1; -
DR EMBL; D38122; BAA07320.1; -
DR EMBL; AF288573; AAG60017.1; -
DR EMBL; Z96050; CAB09424.1; -
DR EMBL; BC017502; AAI17502.1; -
DR EMBL; AB013303; BAA32542.1; -
DR F1R; I38707; I38707.
DR HSSP; P01375; 1TNF.
DR Genew; HGNC:11936; TNFSF6.
DR MIM; 134638; -
DR MIM; 601859; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005102; P:receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.

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GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODom; PD002012; TNF_subf; 1.
DR SMART; SMC0207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00449; TNF_2; 1.
DR Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
KW Alternative splicing; Antigen.
FT CHAIN 1 281
FT CHAIN 130 281
FT DOMAIN 1 80
FT TRANSMEM 81 102
FT DOMAIN 103 281
FT DOMAIN 4 70
FT DOMAIN 45 65
FT SITE 129 130
FT SITE 202 233
FT DISULFID 184 184
FT CARBOHYD 250 250
FT CARBOHYD 260 260
FT VARSPPLIC 117 127
FT FTId=VSP_006443.
FT Missing (in isoform 2).
FT FTId=VSP_006444.
FT P->D,F,R: LOWERS BINDING TO TNFRSF6 AND
FT REDUCES CYTOTOXICITY MORE THAN 100-FOLD.
FT Y->F,R: LOWERS BINDING TO TNFRSF6 AND
FT ABOLISHES CYTOTOXICITY.
FT F->L: ABOLISHES BINDING TO TNFRSF6 AND
FT CYTOTOXICITY.
FT SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;
Query Match 14.2%; Score 182.5; DB 1; Length 281;
Best Local Similarity 27.4%; Pred. No. 6.6e-08;
Matches 57; Conservative 40; Mismatches 70; Indels 41; Gaps 10;
QY 44 WQLRQLVKMI-LRTSEETISTVQEKQNI---SPLVREGRQPVAAHITCTGRSNTLS 99
DB 102 FQLFHLQELAELESTQMTASLEKQIGHPSP-PPEKKELKVAHLT---GKSNSRS 157
QY 100 SPNSKNEKALGRKINSMESSRSGHSFLSNLHRLNGELVIHEKGYIYQTYFRQBEIK 159
DB 158 MP-----LEWEDT-YGIVLLSGVKYKGLVINETGLYFVYKVFYFRGQ----- 200
QY 160 ENTQNDKQVQVIY-KYTSYDPDILLMKASRNS-----CWSKDAEYGLYIYGGIFEL 212
DB 201 --SCNNFLSHKVVNRNSKYPQDLVYMEGQKMSYCTTQGMAR-----SSYLGAVENTL 251
QY 213 KENDRIFVSVTNEHLIDMDHEASPFQAF 240
DB 252 TSADHLXNVSELSLVNFEESQTFFGLY 279
RESULT 10
TNF6_PIG
ID TNF6_PIG STANDARD; PRT; 282 AA.
AC Q9BB88; Q95M04; Q95N10;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE ligand).

```

GN TNFRSF6 OR FASL.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21322533; PubMed=11429161;
 RA Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
 RT "Molecular cloning, characterization, and expression of porcine Fas
 RT ligand (CD95 ligand).";
 RL J. Interferon Cytokine Res. 21:305-312(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Guany bama miniature pig;
 RA Zhu N., Young Y.;
 RT "Molecular cloning and characterization of porcine Fas ligand cDNA.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoid;
 RA Tsuyuki S., Kono M., Bloom E.T.;
 RT "Cloning and potential utility of porcine Fas ligand: overexpression
 RT in porcine cells protects them from attack by human cytolytic cells.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;
 RX MEDLINE=21653191; PubMed=11792426;
 RA Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
 RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison
 RT with human gene.";
 RL Mol. Immunol. 38:581-586(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
 CC modulates its effects (By similarity).
 CC -!- SUBUNIT: Homotrimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- INDUCTION: By IL-18.
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC
 CC EMBL; AB027297; BAB40919.1; -
 CC EMBL; AY036344; AAK56449.1; -
 CC EMBL; AF397407; AAK84408.1; -
 CC EMBL; AB069764; BAB64291.1; -
 CC HSSP; P01375; 4TSV.
 CC InterPro; IPR008064; Fas ligand.
 CC InterPro; IPR006053; TNF_abc.
 CC InterPro; IPR006052; TNF_family.
 CC InterPro; IPR008983; TNF_like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00223; TNF; 1.
 CC PRINTS; PR01681; FASLIGAND.
 CC PRINTS; PR01234; TNFCROSINFCT.
 CC ProDom; PD002012; TNF_subf; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; 1.
 CC PROSITE; PS50049; TNF_2; 1.

KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 282 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CHAIN 131 282 MEMBER 6, MEMBRANE FORM.
 FT CHAIN 131 282 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CHAIN 131 282 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
 FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT TRANSMEM 83 103 (POTENTIAL).
 FT DOMAIN 104 282 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 4 70 PRO-RICH.
 FT DOMAIN 45 56 POLY-PRO.
 FT SITE 130 131 CLEAVAGE (BY SIMILARITY).
 FT DISULFID 203 234 POTENTIAL.
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 5 5 P -> L (IN REF. 4).
 FT CONFLICT 57 57 T -> P (IN REF. 2).
 SQ SEQUENCE 282 AA; 31756 MW; 6743DAA1145671FB CRC64;
 Query Match 14.1%; Score 182; DB 1; Length 282;
 Best Local Similarity 27.1%; Pred. No. 7.2e-08;
 Matches 55; Conservative 37; Mismatches 71; Indels 40; Gaps 9;
 QY 45 QLRQLVRKMLRSTSETISTVQKQNIPLVRERGPQVAAHITGRNSNTLSPNSK 104
 DB 111 ELTELRESASQRHTESL-----EKQIGHPNLPSEKELRKVAHLTG-----XENSR 157
 QY 105 NEXALGRKINSWESSRSGHSLNHLRNGELVIHEKGFYIYSQYFRFOEIKENTKN 164
 DB 158 SIPL-----EWEDT-YGIALVSGVKYMGKSLVINDTGLYFYVSKYVFRGQ-----YCN 204
 QY 165 DKQMVQYIYKYTS-YPPILLMK-SARNSC-----WSKDAEYGLYIYQGGIFELKENDR 217
 DB 205 NQPLSHKAVYTRNSKYPQDLVMEGKMNVCYCTQMMAR-----SSYLGAENVLTASDH 257
 QY 218 IFYVTVNEHLIDMDHEASREGAF 240
 DB 258 LYNVNSELVNFEEKTPFGLY 280
 RESULT 11
 TNF6 RAT STANDARD; PRT; 278 AA.
 ID TNF6 RAT
 AC P36940;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN TNFRSF6 OR FASL OR APTLIG1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94084792; PubMed=7505205;
 RA Suda T., Takahashi T., Golstein P., Nagata S.;
 RT "Molecular cloning and expression of the Fas ligand, a novel member
 RT of the tumor necrosis factor family.";
 RL Cell 75:1169-1178(1993).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
 CC modulates its effects (By similarity).
 CC -!- SUBUNIT: Homotrimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND

THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES, KIDNEY AND LUNG.

-!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.

-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

-!- SIMILARITY: Belongs to the tumor necrosis factor family.

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EMBL; U03470; AAC52129.1; -.

PIR; A49266; A49266.

HSSP; P01375; 4TSV.

InterPro; IPR008064; Fas ligand.

InterPro; IPR006053; TNF_abc.

InterPro; IPR006052; TNF_family.

InterPro; IPR008983; TNF_like.

InterPro; IPR003636; TNF_subf.

Pfam; PF00229; TNF; 1.

PRINTS; PR01681; FASLIGAND.

PROSITE; PS00251; TNF; 1.

PROSITE; PS0049; TNF; 1.

Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

CHAIN 1 278

CHAIN 127 278

DOMAIN 1 77

TRANSMEM 78 99

DOMAIN 100 278

DOMAIN 4 69

DOMAIN 45 58

SITE 126 127

DISULFID 199 230

CARBOHYD 116 116

CARBOHYD 247 247

CARBOHYD 257 257

SEQUENCE 278 AA; 31140 MW; 2898E19A862CEAC6 CRC64;

Query Match 13.8%; Score 177.5; DB 1; Length 278;

Best Local Similarity 27.3%; Pred. No. 1.7e-07;

Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 62 ISTVQKQNPISPLVRGQPVAAHITGT-RGRSNTLSPNSKNEKALGRKINSWESSR 120

Db 121 VSSFEKQNPSTPSTKPRSV-AHLTGNPRSRSLP-----EWEDT- 162

QY 121 SGHSFLNLRLNGELVIHKGPGYYSQYFFQBEIKENTKDKQKQYIY-KYTSYP 179

Db 163 YGTALISGVYKKGGLVINEAGLYFYVSKYFEGQ-----SCNSQLSHKVMYRNFKYP 216

QY 180 DPTLLMKSR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 238

Db 217 GDLVLMEEKLNLYCTT--GGIWAHSSYLGAFFNLTVADHLVNVISQLSLNFEESKTFPG 274

QY 239 AF 240

Db 275 LY 276

RESULT 12

TNFS_CHECK STANDARD; PRT; 272 AA.

ID TNFS_CHECK

AC Q918D8;

28-FEB-2003 (Rel. 41, Created)

15-MAR-2004 (Rel. 43, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).

TNFSF5 OR CD40LG OR CD40L.

Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI_TaxID=9031;

[1]

SEQUENCE FROM N.A.

SRAIN-White leghorn; TISSUE-Spleen;

RA Tregaskes C.A.; Young J.R.; Burnside J.;

FT "Cloning of a putative chicken CD40 ligand.";

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IGE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).

CC -!- SUBUNIT: Homotrimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

CC -!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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EMBL; AJ243435; CAB95748.2; -.

HSSP; P29965; IALY.

GO; GO:0016021; C:Integral to membrane; ISS.

GO; GO:0005174; F:CD40 receptor binding; ISS.

GO; GO:0042100; P:B-cell proliferation; ISS.

GO; GO:0006954; P:Inflammatory response; ISS.

GO; GO:0007159; P:Leukocyte cell adhesion; ISS.

GO; GO:0030188; P:Platelet activation; ISS.

InterPro; IPR003263; TNF_5.

InterPro; IPR006052; TNF_like.

InterPro; IPR008983; TNF_subf.

Pfam; PF00229; TNF; 1.

PRINTS; PR01702; CD40LIGAND.

ProDom; PD008600; TNF_5; 1.

ProDom; PD002012; TNF_subf; 1.

SMART; SM00207; TNF; 1.

PROSITE; PS00251; TNF; 1.

PROSITE; PS0049; TNF; 1.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

CHAIN 1 272

CHAIN 111 272

DOMAIN 1 23

TRANSMEM 24 44

DOMAIN 45 272

SITE 110 111

DISULFID 190 229

CARBOHYD 124 124

CARBOHYD 146 146

CARBOHYD 251 251

SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;

Query Match 13.3%; Score 171; DB 1; Length 272;

Best Local Similarity 25.5%; Pred. No. 5.6e-07;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:53:00 ; Search time 20 Seconds
(without alignments)
1168.727 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKQMDKYKSGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189.5	14.7	279	2 A53062	Fas ligand - mouse
2	182.5	14.2	281	2 I38707	Fas ligand - human
3	177.5	13.8	278	2 A49266	Fas ligand - rat
4	152	11.8	261	2 S3090	CD40 ligand - bovi
5	138.5	10.8	260	2 S21738	CD40 ligand - mous
6	137	10.6	261	2 I3476	CD40 ligand - huma
7	134.5	10.5	204	1 S17289	tumor necrosis fac
8	131.5	10.2	234	1 A25451	tumor necrosis fac
9	130	10.1	232	1 S12606	tumor necrosis fac
10	129.5	10.1	235	2 I54490	tumor necrosis fac
11	127.5	9.9	204	1 S24641	lymphotoxin - bovi
12	126	9.8	234	1 J01344	tumor necrosis fac
13	123	9.6	233	1 QHUN	tumor necrosis fac
14	122	9.5	205	1 QWHUX	lymphotoxin alpha
15	121	9.4	235	1 QWMSN	tumor necrosis fac
16	121	9.4	235	1 J00029	tumor necrosis fac
17	120	9.3	233	1 S22052	tumor necrosis fac
18	117.5	9.1	234	1 JH0529	tumor necrosis fac
19	115.5	9.0	193	2 S06192	tumor necrosis fac
20	114	8.9	202	2 B27303	tumor necrosis fac
21	113.5	8.8	185	2 S2715	tumor necrosis fac
22	113	8.8	233	1 S24642	tumor necrosis fac
23	111.5	8.7	202	1 JH0869	tumor necrosis fac
24	108.5	8.4	306	2 I49139	tumor necrosis fac
25	107	8.3	197	1 JH0309	lymphotoxin-beta
26	105	8.2	638	1 Q0BY2M	tumor necrosis fac
27	102.5	8.0	652	1 I48083	mRNA maturase b14
28	102	7.9	244	2 A46066	amphotropic murine
29	98.5	7.7	233	2 S1686	lymphotoxin beta - tumor necrosis fac

ALIGNMENTS

RESULT 1

Fas ligand - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53062
R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Cell 76, 969-976, 1994
A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation
A:Reference number: A53062; MUID:94181575; PMID:7511083
A:Accession: A53062
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-279 <TAK>
A:Cross-references: GB:U06948; NID:G473564; PIDN:AAA17800.1; PID:G473565

Query Match 14.7%; Score 189.5; DB 2; Length 279;
Best Local Similarity 25.8%; Pred. No. 1.1e-08;
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

QY	45	QLRQIVRKMILRTSEETISTYQEQKQINISPLVRRGQFQVAAHITGRGRSNTLSSPSNK	104
DB	111	ELREFTNQSL-----KVSSPEKQIANPSTPSEKKEPRSV-AHLTG-----NPHSR	154
QY	105	NEKALGRKINSWSSRSGHSLNLHRLNGELVHEKGFYIYSQTYPRQERKENTKN	164
DB	155	SIPL-----EWEDT-YGTALISGVKYKGLVINETGLYFVYSKYVFRGO-----SCN	201
QY	165	DKQMVQYIY-KYTSYPPFILMKSR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVS	222
DB	202	NQPLNHKVMYMSKYPEDLVLMSEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLYVNI	259
QY	223	TNEHLIDMDHEASFGAF	240
DB	260	SQLSLINFESKTFPGLY	277

RESULT 2

Fas ligand - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I38707; J02340; S57585; I38554
R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S. Int. Immunol. 6, 1567-1574, 1994
A:Title: Human Fas ligand: gene structure, chromosomal location and species specificity
A:Reference number: I38707; MUID:95127560; PMID:7826947
A:Accession: I38707
A:Status: preliminary; translated from GB/EMBL/DBU
A:Molecule type: mRNA
A:Residues: 1-281 <RES>
A:Cross-references: EMBL:U11821; NID:G595430; PIDN:AAC50124.1; PID:G595431

30	97.5	7.6	448	2	F95122	protein kinase, pr
31	95	7.4	455	2	G95104	hypothetical prote
32	93	7.2	1465	2	T23056	chromodomain helic
33	92.5	7.2	833	1	A31593	heat shock transcr
34	92.5	7.2	1538	2	T29095	cardiac muscle fac
35	92	7.1	865	2	AB1658	probable membrane
36	91	7.1	345	2	T14707	DNA ligase homolog
37	91	7.1	365	2	T15010	hypothetical prote
38	91	7.1	1176	2	JN0583	myosin-light-chain
39	89.5	7.0	313	2	T03031	NBS-LRR type resis
40	89	6.9	328	2	B59296	alpha-N-arabinofur
41	89	6.9	2278	1	S56274	FAB1 protein - Yea
42	88.5	6.9	611	2	S56278	DNA-directed DNA p
43	88.5	6.9	1425	2	R39303	protein C4788.8 [i
44	88.5	6.9	1675	2	I31473	hypothetical prote
45	88	6.8	826	2	JC5153	mitogen-activated

R;Mita, E.; Hayaishi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:G601892; PID:BA07320.1; PID:gl369902
R;Schatzlein, C.E.
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:G887455; PID:G887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G.J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:G624627; PID:AA050071.1; PID:G624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
A;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 182.5; DB 2; Length 281;
Best Local Similarity 27.4%; Pred. No. 4.4e-08;
Matches 57; Conservative 40; Mismatches 70; Indels 41; Gaps 10;

Qy 44 WQLRQLVKMT-LRTSEITSTVQEKQNI---SPLVRERGQPVAAHIHGTGRNTLS 99
Db 102 PQLFLKELAELESTQMTASLEKQGHPSF-PPEKELKVAHLT---GKNSRS 157
Qy 100 SPNSKNEKALGRKINSWESSRSHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEI 159
Db 158 MP-----LEWEDT-YGIVLLSGVYKKGGLVINETGLYFYVSKYFRGQ--- 200

Qy 160 ENTNRDKQMVYI-KYTSYDPDILLMKARS-----CWSKDAEGLYSIYOGGIFEL 212
Db 201 --SCNNPLSHKVMYRNSKYPQDLVMEGKMSTCTTGQWMA-----SSYLGAVFNL 251

Qy 213 KENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 252 TSADHLVNVSELSLVNFEESQTFGLY 279

RESULT 3
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
R;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family.
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SD>
A;Cross-references: GB:U03470; NID:G440178; PID:AA052129.1; PID:G440179
C;Keywords: glycoprotein; transmembrane protein

Query Match 13.8%; Score 177.5; DB 2; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.2e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

Qy 62 ISTVQEKQNI-SPLVRERGQPVAAHIHGT-GRSNTLSLSPNSKNEKALGRKINSWESSR 120
Db 121 VSSFEKQIANSTPSETKPRSV-AHLTGPNRPSRIPL-----EWEDT- 162

Qy 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEI-KENTKNDKQMVYI-KYTSYP 179
Db 163 YGTALISGVYKKGGLVINEAGLYFYVSKYFRGQ-----SCNSQPLSHKVMYRNFKYP 216

Qy 180 DPILLMKAR-NSCWSKDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 238
Db 217 GDLVLMEEKLNYCTT--GQIWAHSSYLGAVFNLTVADHLVYNISQSLINFEESKTFFG 274

Qy 239 AF 240
Db 275 LY 276

RESULT 4
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
R;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
A;Cross-references: EMBL:Z48469; NID:G732569; PID:CAA88363.1; PID:G732570

Query Match 11.8%; Score 152; DB 2; Length 261;
Best Local Similarity 27.1%; Pred. No. 1.6e-05;
Matches 55; Conservative 39; Mismatches 77; Indels 32; Gaps 10;

Qy 39 CMQVQKQLRQLVRKMLRTSETSTVQEKQNI-SPLVRERGQPVAAHIHGTGRNTLS 98
Db 84 CEIERSRFDLV-KDINQKE-----VKKKEKPFEMHKGDOEPQ-IAAHV-----I 127

Qy 99 SSPNSKNEKALGRKINSWESSRSHSFLSN--LHLRNG-ELVIEHKGFFYYISQTYFRFQ 155
Db 128 SPASKTTSVL-----QW--APKGYTSLNVLVLENGKQLAVKKEQGYIYIYQVTFCSN 180

Qy 156 EBIKENTKNDKQMVYI-KYTSYDPDILLMKARSNSCWSKDAEGLYSIYOGGIFELKEN 215
Db 181 RE-----TLQAPPIASLCLKSPSGSERILLRAANTHSSSKPC--QQQSIHLGGVFELOSG 234

Qy 216 DRIFVSVTNEHLIDMDHEASFFG 238
Db 235 ASVFNVTDPQSQVSHGTGFTSFG 257

RESULT 5
S21738
CD40 ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
R;Accession: S21738
R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, J.; Cosman, D.; Spriggs, M.K.
Nature 357, 80-82, 1992
A;Title: Molecular and biological characterization of a murine ligand for CD40.
A;Reference number: S21738; MUID:92244364; PMID:1374165
A;Accession: S21738
A;Molecule type: mRNA
A;Residues: 1-260 <ARM>
A;Cross-references: EMBL:X65453; NID:G50351; PID:CAA46448.1; PID:G50352
C;Keywords: glycoprotein; transmembrane protein
F;23-46/Domain: transmembrane #status predicted <TMM>
F;47-260/Domain: extracellular #status predicted <EXT>

F:239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.8%; Score 138.5; DB 2; Length 260;
Best Local Similarity 25.1%; Pred. No. 0.00023;
Matches 47; Conservative 37; Mismatches 72; Indels 31; Gaps 8;
QY 39 CQVQKWLRLQVRKMLRTSEETISTVQEKQOONISPLVRERGPORVAAHITGRGRSNTL 98
DB 84 CEEERQEDLVKQITLTK-----EEKENSFENQGRDEDPQIAAHV-----V 126
QY 99 SSPNSKNEKALGRKINSWESSRSGHFLSNL-HLRNG-ELVIEHKGYYIYSQTYFRFOE 156
DB 127 SEANSNAASVL-----QW-AKGGYITMKSNLVLENGKQLTVREGLYVYVTVQVFCNR 180
QY 157 EIKENTKDKQWQVYKYTSYDPDILLMKSRNSCKDAEYGLXSIYOGGIFELKEND 216
DB 181 E-----PSSQRFIVGLWLPKIGSERILLKAAANTHSSSQICEQ-QSVHLGGVFELOQA 234
QY 217 RIFVSVT 223
DB 235 SVFVNT 241

RESULT 6

CD40 ligand - human
N:Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C:Accession: S28017; JH0793; S28852; I53476; S25584; S30593
R:Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Bransch-Andersen, S.; EMBO J. 11, 4313-4321, 1992
A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for A:Reference number: S28017; MUID:93049181; PMID:11385114
A:Accession: S28017
A:Molecule type: mRNA
A:Residues: 1-261 <HOI>
A:Cross-references: EMBL:Z15017; NID:G38483; PIDN:CAA78737.1; PID:G38484
R:Spriggs, M.K.; Amitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T. J. Exp. Med. 176, 1543-1550, 1992
A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin A:Reference number: JH0793; MUID:93094757; PMID:1281209
A:Accession: JH0793
A:Molecule type: mRNA
A:Residues: 1-261 <SPR>
A:Cross-references: GB:X67878; NID:G38411; PIDN:CAA48077.1; PID:G38412
R:Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A. Eur. J. Immunol. 22, 3191-3194, 1992
A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A:Reference number: S26694; MUID:93078854; PMID:1280226
A:Accession: S26694
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <GRA>
A:Cross-references: EMBL:X68550; NID:G37269; PIDN:CAA48554.1; PID:G37270
R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J. P. J. Lett. 315, 259-266, 1993
A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e A:Reference number: S28852; MUID:93138085; PMID:7678552
A:Accession: S28852
A:Molecule type: mRNA
A:Residues: 1-261 <GAU>
A:Cross-references: EMBL:L07414; NID:G180123; PIDN:AAA35662.1; PID:G180124
A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln C:Genetics:
A:Gene: GDB:CD40LG; HUGM1; IMD3
A:Cross-references: GDB:120632; OMIM:308230
A:Map position: Xq26-Xq26
C:Keywords: Glycoprotein; transmembrane protein
F:13-44/Domain: transmembrane #status predicted <TMM>
F:45-261/Domain: extracellular #status predicted <EXT>
F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.6%; Score 137; DB 2; Length 261;
Best Local Similarity 24.6%; Pred. No. 0.00031;
Matches 52; Conservative 38; Mismatches 73; Indels 48; Gaps 11;

QY 39 CQVQKWLRLQVRKMLRTSEETISTVQEKQOONISPLVRERGPORVAAHITGRGRSNTL 98
DB 84 CEEIKSOFEGVDIML-NKEET-----KENSFENQKGDQNPQ-IAAHV-----I 127
QY 99 SSPNSKNEKALGRKINSWESSRSGHFLSNL-HLRNG-ELVIEHKGYYIYSQTYFRFOE 155
DB 128 SEASSTKTVL-----QW-AERGGYITMGSNNLVLENGKQLTVKROGLYIYIAQVTFCSN 180
QY 156 EEIKENT-----KNDKQWQVYKYTSYDPDILLMKSRNSCKDAEYGLXSIYOG 207
DB 181 REASSQAPFFASLCLKSPGRFER-----ILLRAANTHSSAKPC-GQQSIHLG 226
QY 208 GIFELKENDRIFVSVTNEHLIDMDHEASFFG 238
DB 227 GVFELOPGASGVFNVTDPQVSHGTGTFSGF 257

RESULT 7

SI7289
tumor necrosis factor beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: SI7289
R:Kuhnert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U. Gene 102, 171-178, 1991
A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a A:Reference number: SI7289; MUID:91340150; PMID:1874444
A:Accession: SI7289
A:Molecule type: DNA
A:Residues: 1-204 <KU>
A:Cross-references: EMBL:X54859; NID:G2132; PIDN:CAA38638.1; PID:G2133
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match 10.5%; Score 134.5; DB 1; Length 204;
Best Local Similarity 24.7%; Pred. No. 0.00037;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;

QY 63 STVQEKQONISPLVRERGPORVAHITG-----TEGRSNTLSSPNSKNEKALGRKINS 115
DB 42 SAAQPAKQH-PPKHLARGTLKPAHLVGDPTDPSLRWRANT-----DRAFLR---- 88
QY 116 WESSRSGHFLSNLHRLNGELVIEHKGYYIYSQTYFRFOEIKENTKNDKQWQVYIYKY 175
DB 89 -----HGFL-----LSNNLLVPTSGLYFVYSQVVSFSGEGCPKATPTPLVLAHEVQLF 137
QY 176 TS-YPDILLMKSRNSCKDAEYGLXSIYOGIFELKENDRIFVSVTNEHLIDMDHEA 234
DB 138 SSQYFFHVPILSSAKSVCPQPGPW-VRSVIQAVFLITCGDQLSTHTDGTPHLLSPSS 196
QY 235 SFFGAF 240
DB 197 VFFGAF 202

RESULT 8

A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25451; J50727
R:Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, DNA 5, 149-156, 1986

A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rad
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <IT0>
A;Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akita, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1996
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
A;Note: this sequence differs from that shown in having a Gln inserted between residues
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: J50727
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62, 'Q', 63-234 <SHA>
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C;Genetics:
A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-234/Product: tumor necrosis factor #status predicted <MAT>
F;83/Binding site: myristate (Lys) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted

Query Match 10.2%; Score 131.5; DB 1; Length 234;
Best Local Similarity 22.9%; Pred. No. 0.00079;
Matches 50; Conservative 36; Mismatches 79; Indels 53; Gaps 10;

QY 29 PNDESMNSPCQVQKQLRQLVRKMI-LRTSEETISTVOEKQKQINSLVRRGQPRVAAH 87
DB 58 PQEESPN-----LHLVNPVQAVTLRSASRALSD-----KPL-----AH 93
QY 88 ITGTGRNTLSSPNKNEKALGRKINSWESSRSHSFLNLHNGRLVTHXGFFYIY 147
DB 94 VVA-----NPQVEGQ-----QWLSORANALLANGWKLTDNLVPAQGLIY 137
QY 148 SQTYFRFQBEIKENTKNDKQVQYIYKY-TSPYDPFILMKSGARNSCWSKOAEYG-----L 201
DB 138 SQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNKVNLISAISKSPCHRETPPEAPWAWY 192
QY 202 YSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS--FFG 238
DB 193 EPIYLGGVFQLEKGRDLSTEVNQPEYLDLAESGQVYFG 230

RESULT 9
S12606
tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S12606; S17290; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
A;Accession: S12606
A;Molecule type: DNA
A;Residues: 1-232 <DRE>
A;Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
R;Kuhnt, P.; Wuehrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: S17289; MUID:91340150; PMID:197444
A;Accession: S17290

A;Molecule type: DNA
A;Residues: 1-232 <KHU>
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
R;Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murtough, M.P.
submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis
A;Reference number: S18965
A;Accession: S18965
A;Molecule type: mRNA
A;Residues: 1-232 <CHO>
A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain react
A;Reference number: I46659; MUID:90034181; PMID:2478420
A;Accession: I46659
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C;Genetics:
A;Introns: 62/3; 78/1; 93/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted

Query Match 10.1%; Score 130; DB 1; Length 232;
Best Local Similarity 25.1%; Pred. No. 0.0011;
Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;

QY 80 GPORVAHITGRGSRNTLSSPNS---KNEKALGRKINSWESSRSHGHSFLNLHNGRL 136
DB 66 GLSLINFLAQLRSSQTSDFKFAHVAVNVAEGQL--QWQSGYANALLANGVGLKDNOL 123
QY 137 VHEKGFYIYQTYFRFOEEIKEN---TKNDKQVQYIYKYTSPYDPFILMKSGARNSCW 193
DB 124 VVPTDGLYIYQVLFRRGQCPSTNVFLTHTSRIA-----VSQTKVNLISAISKSPCQ 177
QY 194 SK-----DAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEAS--FFG 238
DB 178 RETPEGAERKPNVEPIYLGVLGVFQLEKDRLSAEINLPDYLDFAESQVYFG 228

RESULT 10
I54490
tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C;Accession: I54490
R;Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus 1
A;Reference number: I54490; MUID:92218012; PMID:1348497
A;Accession: I54490
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
A;Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C;Genetics:
A;Gene: PLTNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 10.1%; Score 129.5; DB 2; Length 235;
Best Local Similarity 24.5%; Pred. No. 0.0012;

Lymphokine Res. 7, 175-185, 1988

A>Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A;Reference number: A61478; MUID:88301617; PMID:2841543

A;Accession: A61478

A:Molecule type: protein

A;Residues: 56-79;86-95,'X','97','X','99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',171,PEES Lett 314, 85-88, 1992

R;Voigt, C.G.; Maurer-Peguy, I.; Adolf, G.R.

A>Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylation A;Reference number: S26951; MUID:93083656; PMID:1451807

A;Accession: S26951

A:Molecule type: protein

A;Residues: 35-59,'N',61-205 <VOI>

A;Note: 60-Thr was also found

R;Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K. Arch. Biochem. Biophys. 304, 144-153, 1993

A>Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO A;Reference number: S34742; MUID:93311995; PMID:8323280

A;Contents: annotation

C;Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction, while having no detrimental effect on normal cells. It can also act synergistically with C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of different activities but are produced by different cell types and have different induction kinetics.

C;Genetics:

A;Gene: GDB:LTA; LT; TNFB

A;Cross-references: GDB:I20442; OMIM:153440

A;Map position: 6p21.3-6p21.3

A;Introns: 33/3; 69/1

A;Note: the first intron occurs before the initiator codon

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxicity; glycoprotein; homotrimer; lymphokine; macrophage F;1-34/Domains: signal sequence #status predicted <SIG>

F;25-205/Product: lymphotoxin #status predicted <WAT>

F;41/Binding site: carbohydrate (thr) (covalent) #status experimental

F;96/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 9.5%; Score 122; DB 1; Length 205;
Best Local Similarity 23.4%; Pred. No. 0.0043;
Matches 37; Conservative 29; Mismatches 72; Indels 20; Gaps 5;

Qy 85 AAHTTGRGSRNTLSPNSKNEALGRKINSWRSSRGHSFLSNLHNGELVIHEKGFY 144
Db 64 AAHLIGDPSKQNSL-----LWRANTRAFLQDGFSLSNNSLIVPTSGY 107

Qy 145 YTSQYTFRFEIEIKTKDKQMVIKYYS-YDPILLMKSAARNCSWKDAEGLYS 203
Db 108 FVYSQVFVGSKAYSPKATSSPLYLAEHVQLFSSQYPFHVPLL-SSQQAVYFGLEQPWLHS 166

Qy 204 IQCGGIPELKENDRIFVSVIN-BELIDMDHEASFPFAG 240
Db 167 MYGAALQLTGDDQLSTHTDGPILVL-LSPSTVFFGAF 203

RESULT 15

QWMSN

tumor necrosis factor alpha precursor - mouse

N;Alternate names: cachectin; TNF alpha

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 04-Feb-2000

C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H. DNA 7, 193-201, 1988

A>Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis A;Reference number: A22908; MUID:88224564; PMID:2836146

A;Accession: A22908

A:Molecule type: DNA

A;Residues: 1-235 <SHI>

A;Cross-references: GB:M20155

R;Shakhov, A.N.; Nedospasov, S.A. Bioorg. Khim. 13, 701-705, 1987

A>Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucle A;Reference number: S03791; MUID:87298639; PMID:3040015

A;Accession: S03791

A;Molecule type: DNA
A;Residues: 1-235 <SHA>
A;Cross-references: GB:M83296; NID:g202086; PIDN:AAA040459.1; PID:g202087
R;Note: article in Russian with English abstract
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor i
A;Reference number: A36679; MUID:88067722; PMID:3684584
A;Accession: A27303
A;Molecule type: DNA
A;Residues: 1-235 <SEM>
A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832
R;Penicka, D.; Hayflick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necro
A;Reference number: A25164; MUID:85298296; PMID:3898078
A;Accession: A25164
A;Molecule type: mRNA
A;Residues: 1-235 <PEN>
A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA040458.1; PID:g202085
R;Fransen, L.; Muller, R.; Marmonier, A.; Tavernier, J.; van der Heyden, J.; Kawashim
Nucleic Acids Res. 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic ex
A;Reference number: A32127; MUID:85242112; PMID:2989794
A;Accession: A23127
A;Molecule type: mRNA
A;Residues: 1-235 <GRA>
A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
E;Caeh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul
A;Reference number: A34251; MUID:89380231; PMID:2777790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSE>
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region
A;Reference number: I59058; MUID:86149365; PMID:2415912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-230, X', 232-235 <RES>
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA040457.1; PID:g202083
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor
A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85, X', 87-99 <SHE>
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F:80-235/Product: tumor necrosis factor #status experimental <MAT>
P:20/Binding site: myristate (Iys) (covalent) #status predicted
P:84/Binding site: carbohydrate (ser) (covalent) #status predicted
P:86/Binding site: carbohydrate (Asn) (covalent) #status predicted
P:148-179/Diglycid bonds: #status predicted

Query Match	9.4%;	Score 121;	DB 1;	Length 235;
Best Local Similarity	23.1%;	Pred. No. 0.0063;		
Matches 43;	Conservative 34;	Mismatches 79;	Indels 30;	Gaps 8
Qy	67	EKQNIISPLVERBGPQVAHHITGRSNTLSPP-----NSKNEKALGRKINSWESSR	120	
Db	62	EKFNGPLI-----SSMAQTLTIRSSQNSDKPVAHVAVHQVEQL-----EMLSQR	111	
Qy	121	SGHSFLSNLHNGELVIEHKGFFYVYSQTFFRQEEIKENTKNDKQMVQIYKYT-SYP	179	
Db	112	ANATIANGMIDIKNOLVVPADGLYLVYSOVLFKGO-----GCPDVLLTHTVSRPAISYQ	166	

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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:53:00 ; Search time 46 Seconds
(without alignments)
1666.759 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSGKSIACFL.....NEHLIDMDHEASFFGAFVLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	68.3	287	11	Q8K3G0
2	703.5	54.7	304	13	Q7T1F2
3	307.5	23.9	317	13	Q7ZXX9
4	305.5	23.7	214	13	Q9DDZ5
5	305	23.7	287	13	Q9DWT9
6	184.5	14.3	279	11	Q7TMV9
7	180	14.0	252	11	Q8K3Y8
8	176.5	13.7	280	6	Q861W5
9	175.5	13.6	169	11	Q9WV90
10	175	13.6	252	11	Q80Y20
11	173	13.4	252	11	Q8K3Y7
12	166	12.9	251	4	Q8NFE9
13	157	12.2	154	6	Q8MJ19
14	151.5	11.8	227	13	Q7TQ3
15	144.5	11.2	216	11	O70332
16	141	11.0	231	13	Q8AW02

17	137.5	10.7	232	11	Q80XA4
18	135	10.5	156	11	Q91ZL4
19	135	10.5	215	6	Q9BEE8
20	135	10.5	217	11	Q9ERG6
21	130.5	10.1	222	13	Q7T1U4
22	128	9.9	230	13	Q8G37
23	127	9.9	253	13	Q7T194
24	126.5	9.8	225	13	Q91B42
25	125	9.7	215	11	Q99ND1
26	124	9.6	216	6	Q9BEC4
27	123.5	9.5	216	6	Q9BEC9
28	122	9.5	205	4	Q8N4C3
29	121.5	9.4	225	13	Q91B41
30	121.5	9.4	246	13	Q91976
31	121.5	9.4	246	13	Q91970
32	120	9.3	237	13	Q8AWC9
33	119	9.2	202	11	Q80WE7
34	115.5	9.0	149	6	Q97543
35	113.5	8.8	255	13	Q91810
36	113.5	8.8	255	13	Q9DEP9
37	110.5	8.6	217	6	Q9BEG0
38	110	8.5	93	6	Q9TTU2
39	109.5	8.5	149	6	Q97538
40	109.5	8.5	149	6	Q9TTG8
41	108.5	8.4	214	6	Q9BEP3
42	108	8.4	103	6	Q864Y7
43	108	8.4	217	6	Q9BEG1
44	107	8.3	217	6	Q9BEP4
45	106.5	8.3	102	11	Q80Z06

ALIGNMENTS

RESULT 1

Q8K3G0 PRELIMINARY; PRT; 287 AA.
 ID Q8K3G0
 AC Q8K3G0
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RA Mueller A.M., Giegerich G.;
 RT "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY115578; AAM49797.1;
 DR GO; GO:0015020; C:membrane; IEA.
 DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 68.3%; Score 879; DB 11; Length 287;

Best Local Similarity 59.7%; Pred No. 1.6e-65;

Matches 170; Conservative 25; Mismatches 43; Indels 6; Gaps 2;

QY 2 NELKQMDKYSGKSIACFLKEDSDSWDNDEBSMNSPCWQVQRLVRKMLTSET 61

Db 44 NEVKQLQDNYSKIGLACFSKEDGDFWSDTEGILNRPCLQVKRQLYIEVTLTFT 103

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QY 62 ISTVQKQVIGSPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 121
DB 104 ISTVPEKQLSTPLPRGRPRQVAAHITGTRSNLALIPISKQCKTLGQKLTWESSRR 163
QY 122 GHSFLSNLHRLNGELVHKGFIYYSQYTFRQF--EIKENTKD----KQVQYIYKY 175
DB 164 GHSFLNHLVRLNGELVHKGFIYYSQYTFRQF--EIKENTKD----KQVQYIYKY 223
QY 176 TSPYDPDILLMKARNCSWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHEAS 235
DB 224 TSPYDPDILLMKARNCSWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHEAS 283
QY 236 FFGA 239
DB 284 FFGA 287

RESULT 2
Q7T1F2 PRELIMINARY; PRT; 304 AA.
AC Q7T1F2
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN TRAIL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Syed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;
RT "Identification and Characterization of Chicken TNF-Superfamily
RT Ligand 8 (CD30 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
RT Inducing Ligand TRAIL).";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB114678; BAC79267.1; -.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.7%; Score 703.5; DB 13; Length 304;
Best Local Similarity 54.7%; Pred. No. 8.2e-51;
Matches 141; Conservative 40; Mismatches 58; Indels 19; Gaps 6;

QY 1 TNELKQMDKYKSGIACFLKEDSYWDPN----DESMNSPCWQVKQLRQLVKWL 55
DB 36 TNELKQMDYKSGTACLTGELGDLIQNLVDVESKDRVADFCWQVKHLGLIKKMS 95
QY 56 RTSEETISTVQ-EKQONISPLVRERQ----RVAAHITGRSNTLSPNSKNEKALG 110
DB 96 RILQNNMSAINGDRTOALS-RDEPPQGTALRAAHLTGSKRSSA-SPHNYLSYRGIG 152
QY 111 RKINSWESSRSGHFLNHLRNGELVHKGFIYYSQYTFRQF-----IKENTKN 164
DB 153 HKHSWESSRSGHFLNHLRNGELVHKGFIYYSQYTFRQF-----IKENTKN 212
QY 165 DKQWQVYIYKTSYPPDILLMKARNCSWCKDAEYGLYSYQGGIFELKENDRIFVSVN 224
DB 213 PKQLVQVYIYKLTNYPDILLMKARSARTCSWCKDAEYGLYSYQGVFOLKREDRIFVSVN 272
QY 225 EHLDMDEHSAFFGAFLV 242
DB 273 SDIVDMDEHSAFFGAFLV 290

RESULT 3
Q7ZYX9 PRELIMINARY; PRT; 317 AA.
AC Q7ZYX9
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
```

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DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Similar to tumor necrosis factor (ligand) superfamily, member 10.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044336; AAH44336.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCB9F CRC64;

Query Match 23.9%; Score 307.5; DB 13; Length 317;
Best Local Similarity 29.8%; Pred. No. 1.2e-17;
Matches 77; Conservative 50; Mismatches 96; Indels 35; Gaps 8;

QY 1 TNELKQMDKYKSGIACFLKEDSYWDPN--ESMNSPCWQVKQLRQLVKWL----- 53
DB 73 TEELRCL-----GLNLVLGKQDI--PEDLAQLFGPCMKLAGIKAVISKVTDISI 123
QY 54 ----ILRTSEETISTVQEKQONISPLVRERQVAAHITGRSNT-----LSSPNS 103
DB 124 KQTLHAARTHSTYNTGSKFWTV-----MORPSAHLTSSASNSRPSQDMHQPF 176
QY 104 XNEKALGRKINSWESSRSGHFLNHLRNGELVHKGFIYYSQYTFRQF-QBEIKENT 162
DB 177 DLHQCRRHPVHTW-ANKSFGAHLNMTLTNGLRVPQDGRYIYYSQYTFRPSDSDQS 235
QY 163 KNDKQWQVYIYKTSYPPDILLMKARNCSWCKDAEYGLYSYQGGIFELKENDRIFVSV 222
DB 236 SVSHQLVQCIYKTSYLNPLQLLKGVTGKWPADAEALHSVIOGGLFELRAGDEVFVS 295
QY 223 TNEHLIDMDHEASFFGAF 240
DB 296 SSTWVYGEDSSSYFGAF 313

RESULT 4
Q9DDZ5 PRELIMINARY; PRT; 214 AA.
AC Q9DDZ5
DT 01-NAR-2001 (T-EMBLrel. 16, Created)
DT 01-NAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE TRAIL-like protein.
GN TNFSF10L.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
RT ligands in the fish ovary."
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481 (2001).
DR EMBL; AF250041; AAG47640.1; -.
DR HSSP; P50591; 1DQ.
DR ZFIN; ZFIN-GENE-010801-1; tnfsf10l.
```

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DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match      23.7%; Score 305.5; DB 13; Length 214;
Best Local Similarity 37.6%; Pred. No. 1.1e-17;
Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps 3;

QY 82 QRVAHITGRGRNT-----LSSPNKNEALGRKINSWSSRSGHSLNHLRNGEL 136
DB 47 QAPSAHLTSSASDNSRQSDHQDFDLHSCRPVHTW-ANKSFGAHLNWTLTGRL 105

QY 137 VIHEKGFYIYQTYFRF-QEEIKENTKNDKQMVYIYKTSYPPDLLMKSARNCSWK 195
DB 106 RVPQGRYLYSVQYFRYSPSDSQSSVSHQVQCIYKTSYLNPIQLLKGVTGKWAP 165

QY 196 DAEYGLSYQGGITELKENDRIFVSVTNEHLIDMDHEASPFQAF 240
DB 166 DAYALSHSYQGLPELRAGDEVFVSVPMTVMYGEDSSSYFGAF 210

RESULT 5
Q30WT9 PRELIMINARY; PRT; 287 AA.
ID Q30WT9;
AC Q30WT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057941; AAL23702.1; -.
DR FSSP; O35235; 1IQA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_subf.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32092 MW; DB061C95087B108 CRC64;

Query Match      23.7%; Score 305; DB 13; Length 287;
Best Local Similarity 33.7%; Pred. No. 1.7e-17;
Matches 84; Conservative 40; Mismatches 97; Indels 28; Gaps 8;

QY 8 QDKYSGGIACFLKEDSDYWDNDDESM-NSPCQVQWQLRQLVRKMLRTSEET--ST 64
DB 47 QSQGSSEELRCLQLNQOQSGSLEELISNQC-----LKLANTIKAYATVTENVISRSV 102

QY 65 VQEQKQ---NISP-LVRERGPQVAHH-----TGTRGRSNTLSSPNSKNEKALGR 111
```

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DB 103 VNEAQSYFNISEGQVATKTLGKPSAHLFRPQNPQAQDSSRRFNGLS-----QSCRH 155
QY 112 KINSWESSRSGHSLNHLRNGELVTHEKGFYIYQTYFRFQEEIKENTKNDKQMVY 171
DB 156 AITRWEDS-TIHLQNITYRDLRNVQAGKYVYVSIYFYRSDGAGARVSPQLVQC 214
QY 172 IYKYTSYPPDLLMKSARNCSWKDAEYGLSYQGGITELKENDRIFVSVTNEHLIDMD 231
DB 215 INWKTSYQFILLKGVGTGKWAPEAEYGLHALYQGLFELKAGDELFFVSVSSLAIDYSD 274
QY 232 HEASPFQAF 240
DB 275 AAASYFGAF 283

RESULT 6
Q7TMV9 PRELIMINARY; PRT; 279 AA.
ID Q7TMV9;
AC Q7TMV9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tnsf6 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapellato M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Besak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052866; AAH52866.1; -.
SQ SEQUENCE 279 AA; 31416 MW; C2972E2728FBBB7B CRC64;

Query Match      14.3%; Score 184.5; DB 11; Length 279;
Best Local Similarity 25.3%; Pred. No. 2e-07;
Matches 50; Conservative 51; Mismatches 64; Indels 33; Gaps 9;

QY 45 QLRQLVRKMLRTSEETISTVQEQQNISPLVRERGPQVAHHITGRSNTLSSPNSK 104
DB 111 ELREFTNQSL-----KVSSFQKQIANPSTPKEKPSV-AHUTG-----NPHSR 154

QY 105 NEKALGRKINSWSSRSGHSLNHLRNGELVTHEKGFYIYQTYFRFQEEIKENTKN 164
DB 155 SIPL-----EWDT-YGTALISGVKYKGLVLNETGLYFVSKVYFRGQ-----SCN 201

QY 165 DKQMVQYIY-KYTSYPPDLLMKSAR-NSCWKDAEYGLSYQGGITELKENDRIFVSV 222
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Db 202 NQPLAHKVMRSKYPEDVLMEERLNYCTT--GQIWAHSHLGAVENTLTSADHLVNI 259
QY 223 TNEHLIDMDHEASFFGAF 240
Db 260 SLSLINFESKTFGLY 277

RESULT 7

ID Q8K3Y8 PRELIMINARY; PRT; 252 AA.
AC Q8K3Y8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TL1A.
GN TNFSF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=21909416; PubMed=11911831;
RA Wigone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
Carrell J., Boyd E., Olsen H.S., Hu G., Fukac L.S., Liu D., Ni J.,
Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TL1A is a TNF-like ligand for DR3 and TR6/DR3 and functions as a T
cell costimulator";
RL Immunity 16:479-492(2002).
DR EMBL; AF520786; AA07367.1; -.
DR MGD; MGI:2180140; Tnfslf15.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 252 AA; 27723 MW; BB901C9350119E0F CRC64;

Query Match 14.0%; Score 180; DB 11; Length 252;
Best Local Similarity 32.4%; Pred. No. 4.1e-07;
Matches 69; Conservative 26; Mismatches 80; Indels 38; Gaps 12;

QY 45 QLRLVRLMRLTSEETISTVQKQNIPLVRERGPQVAAHITGRGRSNTLSPNSK 104
Db 63 QLAVPGKDCMLRAITERSB-PSFQVYSP---PRGKPR--AHLT-----IKQTPAPHLX 112
QY 105 NE-KALGRKINSWESSRSGHSFLSN-LHLRNGELVTHEKGFYIYSQTYFRQBEI---- 158
Db 113 NQLSAL-----HWEHD-LGVAFTKMGKYNKSLVIPESGDYFIYSQITFRGTTSYCGDI 166
QY 159 ---KENTKNDKQMVQYIY-KYTSYDPDILLMK-SARNSC-----WSKDAEGLYSIYGGIF 210
Db 167 SRGRPNKPSITVITKVDSPPEPARLLTGSKSVCESINNW-----FQSLYGANF 219
QY 211 ELKENDRIFVSVTNEHLIDMDHE-ASFFGAFV 242
Db 220 SLEEGRLMVNSDISLVDTYKEDKTPFFGAFLL 252

RESULT 8

Q861W5 PRELIMINARY; PRT; 280 AA.
ID Q861W5
AC Q861W5;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas ligand.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99053606; PubMed=9839871;
RA Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Taubota K.,
Mikami I., Ohno K., Matsui T., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of feline Fas antigen and Fas ligand cDNAs";
RL Vet. Immunol. Immunopathol. 65:161-172(1998).
DR EMBL; AB009280; BAC76426.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 280 AA; 31361 MW; 6AA7E2DE1F1A6B5C CRC64;

Query Match 13.7%; Score 176.5; DB 6; Length 280;
Best Local Similarity 26.9%; Pred. No. 9.2e-07;
Matches 56; Conservative 48; Mismatches 63; Indels 41; Gaps 12;

QY 44 WQLRQLVRKMI-LR--TSBETISTVQKQ-QNISPLVRERGPQVAAHITGRGRSNTLS 99
Db 101 FQLFHLQKELAEALRESTSQHVASSLEKQIQLNPPSEKRLKV-AHLTG----- 150
QY 100 SPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIK 159
Db 151 KPNRSRISPL-----EWEDT-YGIALVSGVKYKKGGLVINDTGMFYFYSKVNFRGQ---- 199
QY 160 ENTKNDKQMVQYIY-KYTSYDPDILLMK-SARNSC-----WSKDAEGLYSIYGGIFEL 212
Db 200 --SCNQLPLNHKVTRNSKTPQDLVLNMGKMMYCTTGQWNR-----SSYLGAFFNL 250
QY 213 KENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 251 TSADHLVNVSELSLVSFESSKTFGLY 278

RESULT 9

Q9WV90 PRELIMINARY; PRT; 169 AA.
ID Q9WV90
AC Q9WV90;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas ligand (Fragment).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;

[illegible]

DR InterPro; IPRO03636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 252 AA; 27725 MW; A63ABDCC9E96B0F CRC64;

Query Match 13.6%; Score 175; DB 11; Length 252;
Best Local Similarity 31.9%; Prod.No.1.le-06;
Matches 68; Conservative 26; Mismatches 81; Indels 35; Gaps 12

QY 45 QLRQVRVMIILRTSEETISTVQBKKQNISPVLRRGEQRVAAHITGTRGRSNLTSSPNSK 104
DB 63 QLRVPKGDCMLRAITEERSE--PSGPQQVSP---PRGKPR--AHLT-----IKQTAPHLK 112
QY 105 NF-KALGRKINSWESSRSGHSFLSN-LHLENGELVIHEXGFYYIYSOTYFRQEII---- 159
DB 113 NLSLAL-----HWBEHD-LGWAFTKGMKYINKSLVIPESGDVFYISYIFTRTTSVCGDI 166
QY 159 ---KENTKNDKQMVMQIVYKTYSVDPTILLMKARNSC-----WSKDAAEYGLYSITYQGIGF 210
DB 167 SGRGREPNKPDSTITVTIKVADSYEPARLITGSKVCEISSNW-----FSQLYLGTATF 219
QY 211 ELKENDRIFVSVTNHELIDMDHE-ASTFGAFIV 242
DB 220 SLIEGEDRLMVNVDSISLVDTYKEDKTFFGAFL 252

RESULT 11
O8K3Y7 PRELIMINARY; PRT; 252 AA.

ID O8K3Y7 PRELIMINARY; PRT; 252 AA.

AC O8K3Y7; AC O8K3Y7; MEDLINE=21509416; PubMed=11911831;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TLIA.
GN TNFSF15.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21509416; PubMed=11911831;
RA Magone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
SA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakara J.P.,
FA Carrell J., Boyd E., Olsen H.S., Hu G., Fukac L., Liu D., Ni J.,
KA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TLIA is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
cell costimulator";
RI Immunity 16:479-492(2002).
RL EWEL; AF520787; RAM77368.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PSS0049; TNF_2; 1.
SQ SEQUENCE 252 AA; 28029 MW; 7789EG65546D46F293 CRC64;

Query Match 13.4%; Score 173; DB 11; Length 252;
Best Local Similarity 32.7%; Pred. No. 1.6e-06;
Matches 55; Conservative 23; Mismatches 62; Indels 30; Gaps 8
QY 86 AHITGTGRSNLTSSPNSKNEKALORKINSSSRSGHSFLSN-LHUNGELVIEHKGFY 144


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Db 98 AHLTINR-----QTPVPHLNKELA-----ALHWNEN-LGMAFTKRMVNTNKNFLVIFESGDY 148
QY 145 YIYSQYFFRFQ-----BEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSC-----192
Db 149 FYISQTFGTWSECODISRVRRPKDPDSITVITKVDADSYEPHAHLITGTKSCVISESN 208
QY 193 WSKDAEYGYISYQGGIFELKENDRIFVSVTNEHLIDMDHE-ASFFGAFLV 242
Db 209 W-----FQPIYLGAMFSLSEEDRLMNVNSDISLVDYTKEDKTFFGAFLI 252

RESULT 12
Q8MJ19 PRELIMINARY; PRT; 251 AA.
AC Q8MF9;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TLIA.
GN TNFSF15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE21909416; PubMed11911811;
RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Peng P., Moore P.A., Ruben S.M., Wei P.;
RT "TLIA is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
RT cell costimulator";
RL Immunity 16:479-492(2002).
DR EMBL; AF520785; AAM77366.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 251 AA; 28087 MW; 65ED70E367E3446D CRC64;

Query Match 12.9%; Score 166; DB 4; Length 251;
Best Local Similarity 33.2%; Pred. No. 6.1e-06;
Matches 62; Conservative 30; Mismatches 65; Indels 30; Gaps 12;
QY 69 QQNISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNE-KALGKINSWESSRSGHSFLS 127
Db 82 QQVAPLRADGDKPR--AHLTVVR-----QPTGQKRNQFPAL-----HWE-HELGLAFTK 129
QY 128 N-LHLRNGELVIHEKGPYIYSQTYFRFQ---BEIKENTKNDK--QMVQIYKYT-SYP 179
Db 130 NRMNYTNKFLLPESGDYFYVSQVTPRGMTSECSIRQAGRPKNKPSITWIKVTDTSYP 189
QY 180 DPILLMKSARNSCWSDAEGV---LVSIIYGGIFELKENDRIFSVTNEHLIDMDHE-AS 235
Db 190 EPTOLLNGTGSVC-----EVGSNWFQPIYLGAMFSLQEGDKLMVNSDSLVDYTKEDKT 244
QY 236 FFGAFLV 242
Db 245 FFGAFLL 251

RESULT 13
Q8MJ19 PRELIMINARY; PRT; 154 AA.
AC Q8MJ19;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Fas ligand CD178 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaquier J.;
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530076; AAM95836.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007155; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 17410 MW; 971A43779E029449 CRC64;

Query Match 12.2%; Score 157; DB 6; Length 154;
Best Local Similarity 27.4%; Pred. No. 1.9e-05;
Matches 46; Conservative 33; Mismatches 65; Indels 24; Gaps 6;
QY 57 TSEETISTVQEQQNISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 116
Db 8 TSQKHTASSLEKQIGHPSPPEKKEQKVAHLTG-----KPNRSRML-----EW 52
QY 117 ESSRSRSHSFLNHLRNGELVIHEKGPYIYSQTYFRFQEIKEKNTKNDKQMVQIY-KY 175
Db 53 EDT-YGIVLLSGVKYKGGVLINETGLYFVYSKYVFRGQ-----SCTNLP LSHKVTWRN 105
QY 176 TSYDPDPILLMKSARNSCWSDAEGVLYSIYQGGIFELKENDRIFSVVT 223
Db 106 SKYPQDLVMWEGKMS-YCTTGQWVAHSSVILGAVFNLTSDHLVNVYS 152

RESULT 14
Q7T2Q3 PRELIMINARY; PRT; 227 AA.
AC Q7T2Q3;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Tumor necrosis factor-3 alpha.
GN TNF-3ALPHA.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Saven R., Sakai M.;
RT "Cloning of tumor necrosis factor 3 alpha in carp."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB112424; BAC77690.1;
SQ SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;
Query Match 11.8%; Score 151.5; DB 13; Length 227;
Best Local Similarity 25.3%; Pred. No. 8.7e-05;
Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7;
QY 75 LVREGRGPORVAHITGTGRNTLLSPNSKNEKALGRKINSWESSRCHSFLSLNHLRNG 134
DB 67 LSKENVTSKVAIHLSGA-----YEPDVSKNNIDWKQNDQGAFAVSGGLKLVD 113
QY 135 ELVIHEKGFYIYSGTYFRFOEIKENTKNDKQMVQIYKYTSYD-----PILLMKSA 188
DB 114 EIIIPNDGIYFIYSQVSPHI--SKNDMTEDQEVNHSVAVFYHSDFFGIYKP--LIRAA 169
QY 189 RNSCW---SKDAEXGLYIYOGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
DB 170 RSACVHASNTEDVWD--TIYLGAFSLRAGDKLCTKTITELLPRVETDNAKTFGVF 225

RESULT 15

O70332
ID O70332 PRELIMINARY; PRT; 216 AA.
AC O70332;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis."
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL: AF046215; AAC40100.1;
DR HSP; P06804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNFCROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS0049; TNF 2; 1.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23793 MW; BADA3F83F45B533 CRC64;

Query Match 11.2%; Score 144.5; DB 11; Length 216;
Best Local Similarity 26.9%; Pred. No. 0.00032;
Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;

QY 80 GPORVAH---ITGTRGRNTL--SSPNSKNEKALGRKINS-----WESSRCHSFLS 127
DB 49 GPQREKFPNPIGSGQTLTRSSQNSNDKPFVGHVAVHQBVEQLEWLSHRANALIAN 108

QY 128 NLHLNGELVIEHEKGFYIYSGTYFRFOEIKENTKNDKQMVQIYK-----VTSYD 180
DB 109 GMSLKDNQIVIPADGLIYVYSQLFRGQ-----GCPSYVLLTHTVSRIVASYED 157
QY 181 PILLMKSAENSCWSKDAEYGV-----LYSIYOGGIFELKENDRIFVSVTNEHLID 229
DB 158 NVNLLISAISKSPC-PKETPEGEELKPYEPIYLGGVFQLEKGDRLSAENVLPKYLD 211

Search completed: June 3, 2004, 08:55:46
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 11:29:46 ; Search time 48 Seconds
(without alignments)
1424.277 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMDKYSKSGTACFL.....NEHLIDMDHEASFFCAFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	279	13	US-10-066-209-3
2	1287	100.0	281	8	US-08-916-625B-6
3	1287	100.0	281	8	US-08-971-317A-8
4	1287	100.0	281	9	US-09-813-329-17
5	1287	100.0	281	9	US-09-193-663-8
6	1287	100.0	281	9	US-09-934-455-1
7	1287	100.0	281	10	US-09-919-039-118
8	1287	100.0	281	12	US-10-202-062-20
9	1287	100.0	281	12	US-10-662-429-2
10	1287	100.0	281	12	US-10-662-430-2
11	1287	100.0	281	12	US-10-662-431-2
12	1287	100.0	281	12	US-10-652-244-2
13	1287	100.0	281	12	US-10-279-687-8
14	1287	100.0	281	13	US-10-039-785-66
15	1287	100.0	281	13	US-10-011-125-4

16	1287	100.0	281	13	US-10-001-054-54
17	1287	100.0	281	14	US-10-093-766-54
18	1287	100.0	281	14	US-10-174-654-11
19	1287	100.0	281	14	US-10-151-882-41
20	1287	100.0	281	14	US-10-218-547-20
21	1287	100.0	281	14	US-10-322-673-72
22	1287	100.0	281	14	US-10-139-785-66
23	1287	100.0	281	14	US-10-310-793-26
24	1287	100.0	281	15	US-10-292-486-5
25	1287	100.0	281	15	US-10-333-712-1
26	1078.5	83.8	246	9	US-09-855-544A-13
27	988	76.8	253	12	US-10-652-244-11
28	988	76.8	256	12	US-10-652-244-13
29	984	76.5	461	12	US-10-389-223A-6
30	982	76.3	480	12	US-10-389-223A-4
31	978	76.0	614	12	US-10-389-223A-2
32	964.5	74.9	296	14	US-10-185-425-5
33	887	68.9	168	9	US-09-900-530A-10
34	878	68.2	166	9	US-09-779-050A-16
35	863	67.1	291	10	US-09-873-829-6
36	863	67.1	291	12	US-10-652-244-6
37	863	67.1	291	13	US-10-017-910-6
38	859	66.7	164	13	US-10-116-378-29
39	850	66.0	161	14	US-10-216-074-7
40	849	66.0	161	14	US-10-338-083-11
41	826	64.2	208	9	US-09-855-544A-16
42	746.5	58.0	188	9	US-09-855-544A-14
43	636	49.4	172	9	US-09-779-050A-17
44	446	34.7	85	14	US-10-286-696-12
45	370	28.7	113	9	US-09-855-544A-15

ALIGNMENTS

RESULT 1
US-10-066-209-3
; Sequence 3, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-3

Query Match 100.0%; Score 1287; DB 13; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSKSGTACFLKEDDSYDPNDESNMSPCWQVKQRLQVRKMLRTSBE 60
Db 37 TNELKQMDKYSKSGTACFLKEDDSYDPNDESNMSPCWQVKQRLQVRKMLRTSBE 96
QY 61 TISTVQEKQNTSPLVREPGPQVAHITGTGRNTLSSPNKKEKALGRINKWESSR 120

Db 97 TISTVQEQKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 180
Db 157 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 216
QY 181 PILLKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 217 PILLKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
QY 241 LVG 243
Db 277 LVG 279

RESULT 2

US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916.625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-625B-6

Query Match 100.0%; Score 1287; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDDESNNSPCWQVKQLRQVLRKMLRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYDNDDESNNSPCWQVKQLRQVLRKMLRTSEE 98
QY 61 TISTVQEQKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEQKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 180
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 218
QY 181 PILLKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 3

US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971.317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mini C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8

Query Match 100.0%; Score 1287; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDDESNNSPCWQVKQLRQVLRKMLRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYDNDDESNNSPCWQVKQLRQVLRKMLRTSEE 98
QY 61 TISTVQEQKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEQKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 180

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Db 159 SCHSFLSNLHLRNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYPD 218
Qy 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281

RESULT 4
US-09-813-329-17
; Sequence 17, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-17

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 98
Qy 61 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
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Db 159 SCHSFLSNLHLRNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYPD 218
Qy 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281

RESULT 5
US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
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; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 98
Qy 61 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
Qy 121 SCHSFLSNLHLRNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYPD 180
Db 159 SCHSFLSNLHLRNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYPD 218
Qy 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281

RESULT 6
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 98
Qy 61 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
Qy 121 SCHSFLSNLHLRNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYPD 180
Db 159 SCHSFLSNLHLRNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYPD 218
Qy 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281
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RESULT 7
US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CDI
US-09-919-039-118

Query Match 100.0%; Score 1287; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVREGRPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVREGRPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRANGELVIEHKGFIYISQTYFRFOEIKENTKNDKQMVYIYKTSYD 180
DB 159 SGHSFLSNLHLRANGELVIEHKGFIYISQTYFRFOEIKENTKNDKQMVYIYKTSYD 218

QY 181 PILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 8
US-10-202-062-20
; Sequence 20, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-202-062-20

Query Match 100.0%; Score 1287; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVREGRPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVREGRPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRANGELVIEHKGFIYISQTYFRFOEIKENTKNDKQMVYIYKTSYD 180
DB 159 SGHSFLSNLHLRANGELVIEHKGFIYISQTYFRFOEIKENTKNDKQMVYIYKTSYD 218

QY 181 PILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 9
US-10-662-429-2
; Sequence 2, Application US/10662429
; Publication No. US20040038347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,429
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-429-2

Query Match 100.0%; Score 1287; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 98
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QY 61 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 180
 Db 159 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 218
 QY 181 PILLMKSARNCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 Db 219 PILLMKSARNCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

RESULT 10
 US-10-662-430-2
 ; Sequence 2, Application US/10662430
 ; Publication No. US20040048340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule I
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/662.430
 ; FILING DATE: 16-Sep-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816.981
 ; FILING DATE: 13-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kimball, Paul, C.
 ; REGISTRATION NUMBER: 34,610
 ; REFERENCE/DOCKET NUMBER: PF261
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-662-430-2

Query Match 100.0%; Score 1287; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESMNSPCWQKQLRQLVRKMLRTSEE 60
 Db 39 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESMNSPCWQKQLRQLVRKMLRTSEE 98
 QY 61 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 180
 Db 219 PILLMKSARNCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

Db 159 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 218
 QY 181 PILLMKSARNCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 Db 219 PILLMKSARNCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

RESULT 11
 US-10-662-431-2
 ; Sequence 2, Application US/10662431
 ; Publication No. US20040047864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule I
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/662.431
 ; FILING DATE: 16-Sep-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816.981
 ; FILING DATE: 13-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kimball, Paul, C.
 ; REGISTRATION NUMBER: 34,610
 ; REFERENCE/DOCKET NUMBER: PF261
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-662-431-2

Query Match 100.0%; Score 1287; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESMNSPCWQKQLRQLVRKMLRTSEE 60
 Db 39 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESMNSPCWQKQLRQLVRKMLRTSEE 98
 QY 61 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 180
 Db 159 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 218
 QY 181 PILLMKSARNCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

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Db 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
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Db 279 LVG 281

RESULT 12
US-10-652-244-2
; Sequence 2, Application US/10652244
; Publication No. US20040052789A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-652-244-2

Query Match 100.0%; Score 1287; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 60
    |||
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 98
    |||
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSR 120
    |||
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSR 158
    |||
Qy 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPD 180
    |||
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPD 218
    |||
Qy 181 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
    |||
Db 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
    |||
Qy 241 LVG 243
    |||
Db 279 LVG 281

RESULT 13
US-10-279-687-8
; Sequence 8, Application US/10279687
; Publication No. US20030211509A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
```

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; FILE REFERENCE: 6255.US.C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-687-8

Query Match 100.0%; Score 1287; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 60
    |||
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 98
    |||
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSR 120
    |||
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSR 158
    |||
Qy 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPD 180
    |||
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPD 218
    |||
Qy 181 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
    |||
Db 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
    |||
Qy 241 LVG 243
    |||
Db 279 LVG 281

RESULT 14
US-10-039-785-66
; Sequence 66, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66

Query Match 100.0%; Score 1287; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 60

Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQNISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEKQNISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDP 180

Db 159 SGHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDP 218

QY 181 PILLMKSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 219 PILLMKSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243

Db 279 LVG 281

RESULT 15

US-10-011-125-4

; Sequence 4, Application US/10011125

; Publication No. US20020142388A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Christina Yu-Ching

; TITLE OF INVENTION: BACTERIAL HOST STRAINS

; FILE REFERENCE: P1804R1

; CURRENT APPLICATION NUMBER: US/10/011.125

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: US 60/256,162

; PRIOR FILING DATE: 2000-12-14

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 4

; LENGTH: 281

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-011-125-4

Query Match 100.0%; Score 1287; DB 13; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.9e-115;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 60

Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQNISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEKQNISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDP 180

Db 159 SGHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDP 218

QY 181 PILLMKSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 219 PILLMKSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243

Db 279 LVG 281

RESULT 16

US-10-001-054-54

; Sequence 54, Application US/10001054

; Publication No. US20020192209A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Baker, Kevin

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Hebert, Carolyn

; APPLICANT: Henzel, William

; APPLICANT: Kabakoff, Rhona

; APPLICANT: Shelton, David

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC

; FILE REFERENCE: P3034R1PCT

; CURRENT APPLICATION NUMBER: US/10/001.054

; CURRENT FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/079920

; PRIOR FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: 60/082999

; PRIOR FILING DATE: 1998-04-24

; PRIOR APPLICATION NUMBER: 60/083545

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/085149

; PRIOR FILING DATE: 1998-05-12

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/088858

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: 60/090691

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/096891

; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: 60/096894

; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: 60/099803

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/100263

; PRIOR FILING DATE: 1998-09-14

; PRIOR APPLICATION NUMBER: 60/100390

; PRIOR FILING DATE: 1998-09-15

; PRIOR APPLICATION NUMBER: 60/101476

; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: 60/107783

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: 60/108849

; PRIOR FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 60/112420

; PRIOR FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: 60/113296

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: 60/115554

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/115558

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/115533

; PRIOR FILING DATE: 1999-01-20

; PRIOR APPLICATION NUMBER: 60/123618

; PRIOR FILING DATE: 1999-03-10

; PRIOR APPLICATION NUMBER: 60/131294

; PRIOR FILING DATE: 1999-04-07

; PRIOR APPLICATION NUMBER: 60/140650

; PRIOR FILING DATE: 1999-06-22

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; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
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; PRIOR FILING DATE: 2000-03-03
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; PRIOR FILING DATE: 1998-11-19
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; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/866034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/882636
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/08615
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28634
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/30095

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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00376
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/22031
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match      100.0%; Score 1287; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TNELKQMDKYKSGIACFLKEDDSYWDNDDESNPCWQVKWQLRQLVRKMLRTSEE 60
Db      39  TNELKQMDKYKSGIACFLKEDDSYWDNDDESNPCWQVKWQLRQLVRKMLRTSEE 98
Qy      61  TISTVOEKQNTISPLVRERGQORVAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 120
Db      99  TISTVOEKQNTISPLVRERGQORVAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 158
Qy      121 SGHSFLSNLHLRNGELVIEHKGFFYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYD 180
Db      159 SGHSFLSNLHLRNGELVIEHKGFFYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYD 218
Qy      181 PILLKMSARNSCWSCDAEYGLYSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

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|||||
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
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Db 279 LVG 281

RESULT 17
US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVKMLRTSEE 60
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVKMLRTSEE 98

QY 61 TISTVQEKQNIPLVREERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNIPLVREERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 180
Db 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 218

QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
|||
Db 279 LVG 281

RESULT 18
US-10-174-654-11
; Sequence 11, Application US/10174654
; Publication No. US20030044937A1
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA

|||||
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
|||
Db 279 LVG 281

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVKMLRTSEE 60
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVKMLRTSEE 98

QY 61 TISTVQEKQNIPLVREERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNIPLVREERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 180
Db 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 218

QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
|||
Db 279 LVG 281

RESULT 19
US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PFS54
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-41
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Query Match
Best Local Similarity 100.0%; Score 1287; DB 14; Length 281;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDSYWDPNDEESMNSPCQVKQLRQVVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDSYWDPNDEESMNSPCQVKQLRQVVKMLRTSEE 98
QY 61 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SCHSFLSNLHNLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVYIKYTSYDP 180
DB 159 SCHSFLSNLHNLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVYIKYTSYDP 218
QY 181 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 20
US-10-218-547-20
; Sequence 20, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-218-547-20

Query Match
Best Local Similarity 100.0%; Score 1287; DB 14; Length 281;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDSYWDPNDEESMNSPCQVKQLRQVVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDSYWDPNDEESMNSPCQVKQLRQVVKMLRTSEE 98
QY 61 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SCHSFLSNLHNLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVYIKYTSYDP 180
DB 159 SCHSFLSNLHNLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVYIKYTSYDP 218
QY 181 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 21
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDSYWDPNDEESMNSPCQVKQLRQVVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDSYWDPNDEESMNSPCQVKQLRQVVKMLRTSEE 98
QY 61 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SCHSFLSNLHNLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVYIKYTSYDP 180
DB 159 SCHSFLSNLHNLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVYIKYTSYDP 218
QY 181 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 22
US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044

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; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66

Query Match      100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQKWLQRLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQKWLQRLVRKMLRTSEE 98

Qy 61 TISTVQEKQONISPLVREERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLNLHLRNGELVHEKGFYIYSQYFRFQEEIKENTKNDKQWQVYIYKTSYDP 180
Db 159 SGHSFLNLHLRNGELVHEKGFYIYSQYFRFQEEIKENTKNDKQWQVYIYKTSYDP 218

Qy 181 PILLMKSARNCSWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243
Db 279 LVG 281

RESULT 23
US-10-793-793-26
; Sequence 26, Application US/10310793
; Publication No. US2003019864A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
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; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26

Query Match      100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQKWLQRLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQKWLQRLVRKMLRTSEE 98

Qy 61 TISTVQEKQONISPLVREERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLNLHLRNGELVHEKGFYIYSQYFRFQEEIKENTKNDKQWQVYIYKTSYDP 180
Db 159 SGHSFLNLHLRNGELVHEKGFYIYSQYFRFQEEIKENTKNDKQWQVYIYKTSYDP 218

Qy 181 PILLMKSARNCSWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243
Db 279 LVG 281

RESULT 24
US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532P1
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-292-486-5

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Query Match      100.0%; Score 1287; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRRGPQRYAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRRGPQRYAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQYFRFQEEIKENTKNDKQWQYIYKYTSYDP 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQYFRFQEEIKENTKNDKQWQYIYKYTSYDP 218
QY 181 PILLMKSGARNSCWSKDAEYGLYSIQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSGARNSCWSKDAEYGLYSIQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281
```

RESULT 25

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US-10-333-712-1
; Sequence 1, Application US/10333712
; Publication No. US20040005314A1
; GENERAL INFORMATION:
; APPLICANT: Escandon, Enrique
; APPLICANT: Fox, Judith A.
; APPLICANT: Kelley, Sean K.
; APPLICANT: Xiang, Hong
; TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
; FILE REFERENCE: P1838R1
; CURRENT APPLICATION NUMBER: US/10/333,712
; PENDING FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: PCT/US01/23691
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,256
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-333-712-1
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Query Match      100.0%; Score 1287; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRRGPQRYAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRRGPQRYAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQYFRFQEEIKENTKNDKQWQYIYKYTSYDP 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQYFRFQEEIKENTKNDKQWQYIYKYTSYDP 218
QY 181 PILLMKSGARNSCWSKDAEYGLYSIQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSGARNSCWSKDAEYGLYSIQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
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Db

279 LVG 281

Search completed: June 3, 2004, 11:36:41
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 09:00:51 ; Search time 20 Seconds
(without alignments)
1168.727 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281
Perfect score: 1287
Sequence: 1 INELKQMDKYKSGIACFL.....NEHLIDMDHASFAGPLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 125680

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134.5	10.5	204	1 S17289	tumor necrosis fac
2	131.5	10.2	234	1 A25451	tumor necrosis fac
3	130	10.1	232	1 S12606	tumor necrosis fac
4	129.5	10.1	235	2 I54490	tumor necrosis fac
5	127.5	9.9	204	1 S24641	lymphotoxin - bovi
6	126	9.8	234	1 JQ1344	tumor necrosis fac
7	123	9.6	233	1 QWJUN	tumor necrosis fac
8	122	9.5	205	1 QWJUX	lymphotoxin alpha
9	121	9.4	235	1 QWJMN	tumor necrosis fac
10	121	9.4	235	2 JU0029	tumor necrosis fac
11	120	9.3	233	1 S22052	tumor necrosis fac
12	117.5	9.1	234	1 JH0529	tumor necrosis fac
13	115.5	9.0	193	2 S06192	tumor necrosis fac
14	114	8.9	202	1 B27303	tumor necrosis fac
15	113.5	8.8	185	2 S52715	tumor necrosis fac
16	113	8.8	233	1 S24642	tumor necrosis fac
17	111.5	8.7	202	1 JH0869	tumor necrosis fac
18	107	8.3	197	1 JH0309	tumor necrosis fac
19	98.5	7.7	233	2 S11688	tumor necrosis fac
20	80.5	6.3	203	2 C89803	hypothetical prote
21	78	6.1	202	2 A82076	conserved hypothet
22	77	6.0	223	2 H71485	hypothetical prote
23	76.5	5.9	195	2 S77753	peptide transport
24	75.5	5.9	142	2 B87569	dnax suppressor pr
25	74	5.7	201	2 B82310	hypothetical prote
26	73	5.7	223	2 B64396	hypothetical prote
27	73	5.7	227	2 B70438	hypothetical prote
28	72.5	5.6	112	2 AF0347	conserved hypothet
29	72.5	5.6	123	2 T26862	hypothetical prote

ALIGNMENTS

RESULT 1

S17289
tumor necrosis factor beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S17289
R:Kuhnert, P.; Wuehrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative an
A:Reference number: S17289; MUID:91340150; PMID:1874444
A:Accession: S17289
A:Molecule type: DNA
A:Residues: 1-204 <XU>
A:Cross-references: EMBL:X54859; NID:G2132; PIDN:CAA38638.1; PID:G2133
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytotoxin; glycoprotein; lymphokine; macrophage
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match	10.5%	Score 134.5;	DB 1;	Length 204;
Best Local Similarity	24.7%	Pred. No. 0.00037;		
Matches	46;	Conservative	31;	Mismatches 76;
				Indels 33;
				Gaps 7;
Qy	63	STVQEKQNISPLVRRBGPORVAHITG-----TGRSNTLSPNSKNEKALGRKINS	115	
Db	42	SAAQPAQH-PPKHLARGTLKPAHLVGDPSTPDSLWRANT-----DRAFLR----	88	
Qy	116	WESSRSGHSLNHLNGLVTHEKGFYIYQTVFRQEEIKENTDKQMVQIYKY	175	
Db	89	-----HGFL-----LSNLSLVPTGLYFYVSQVVFSGGCPFKATPTPLYLAHEVOLF	137	
Qy	176	TS-YPDPILLKMGARNSKDAEYGLYIYQGGIPELKENDRIFSVNTNEHLIDMDHEA	234	
Db	138	SSQYFFVPLLSACKSVCPGQGPW-VRSYVQAVFLLTQGDQLSTHTDTPHLLSPSS	196	
Qy	235	SFFGAP 240		
Db	197	VFFGAP 202		

RESULT 2

A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25451; J05072
R:Rito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi,
DNA 5, 149-156, 1986
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for

A:Reference number: A25454; MUID:86219711; PMID:3519137
A:Accession: A25454
A:Molecule type: mRNA
A:Residues: 1-234 <TO>
A:Cross-references: GB:M12845; NID:G165759; PIDN:AAA31486.1; PID:G165760
R:Itc, H.; Shirai, A.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A:Reference number: A25451; MUID:86219712; PMID:3519138
A:Accession: A25451
A:Molecule type: DNA
A:Residues: 1-234 <T2>
A:Note: this sequence differs from that shown in having a Gln inserted between residues
R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
A:Reference number: JH0309; MUID:91065534; PMID:2249779
A:Accession: J50727
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62, Q, 63-234 <SHA>
A:Cross-references: GB:M60340; GB:M35326; NID:G165754; PIDN:AAA31484.1; PID:G165756
C:Genetics:
A:Introns: 62/3; 80/1; 96/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F:1-81/Domain: propeptide #status predicted <PRO>
F:82-234/Product: tumor necrosis factor #status predicted <MAT>
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:147-178/Disulfide bonds: #status predicted

Query Match 10.2%; Score 131.5; DB 1; Length 234;
Best Local Similarity 22.9%; Pred. No. 0.00079; Mismatches 79; Indels 53; Gaps 10;
Matches 50; Conservative 36; Mismatches 79; Indels 53; Gaps 10;
QY 29 PNDESMNQVQWQKQLRQKMI-LRTSETTSTVOEKQONISPLVREGRGQVAAH 87
DB 58 PQEESFPNN-----LHLNPNVAQVMTLSASRALSD-----KPL-----AH 93
QY 88 ITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKGFYIY 147
DB 94 VVA-----NPFVQGL-----QWLSORANALLANGMKLTQNLVVPADGLYLY 137
QY 148 SQTFFQBEIKENTKNDQMVIYKY-TSPYDPDILMKSNRNSWCKDAEYQ-----L 201
DB 138 SQVLFSGQ-----GCRSYVLLTHTVSRFAVYFNKNLLSAIKSPCHRETPAEAPMAY 192
QY 202 YIIQGGIFELKENDRIFVSVTNEHLIDMDHEAS-PFG 238
DB 193 EPIYLGGVFQLEKGRDLSTEVNQPEYLDLAESQVYFG 230

RESULT 3
S12606
tumor necrosis factor alpha precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S12606; S17290; S18965; I46659
R:Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A:Title: Gene sequence of porcine tumor necrosis factor alpha.
A:Reference number: S12606; MUID:91016861; PMID:2216741
A:Accession: S12606
A:Molecule type: DNA
A:Residues: 1-232 <DRE>
A:Cross-references: EMBL:X54001; NID:G2135; PIDN:CAA37949.1; PID:G2136
R:Kuhmert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A:Reference number: S17289; MUID:91340150; PMID:1874444
A:Accession: S17290
A:Molecule type: DNA

A:Residues: 1-232 <KUH>
A:Cross-references: EMBL:X54859; NID:G2132; PIDN:CAA38639.1; PID:G2134
A:Note: the authors translated the codon GAG for residue 202 as Gly
R:Choi, C.S.; Molitor, T.W.; Lin, G.F.; Muraugh, M.P.
submitted to the EMBL Data Library, January 1991
A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis
A:Reference number: S18965
A:Accession: S18965
A:Molecule type: mRNA
A:Residues: 1-232 <CHO>
A:Cross-references: EMBL:X57321; NID:G2137; PIDN:CAA40591.1; PID:G2138
R:Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reacti
A:Reference number: I46659; MUID:90034181; PMID:2478420
A:Accession: I46659
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 44-232 <PAU>
A:Cross-references: GB:M29079; NID:G164694; PIDN:AAA31128.1; PID:G164695
C:Genetics:
A:Introns: 62/3; 78/1; 93/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F:1-77/Domain: propeptide #status predicted <PRO>
F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:144-176/Disulfide bonds: #status predicted

Query Match 10.1%; Score 130; DB 1; Length 232;
Best Local Similarity 25.1%; Pred. No. 0.0011;
Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;
QY 80 GPORVAAHITGRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGEL 136
DB 66 GPLSINPLAQLRSSSQTSDKPVAVVAVVAKBQL--QWQSGYANALLANGVKKDNOL 123
QY 137 VIHEKGFYIYQTYRFFQBEIKEN--TKNDQMVIYKYTSYDPDILMKSNRNSW 193
DB 124 VPTDGLYIYQVLPFGQCCPSTNVLTHTSRIA-----VSYTKNLLSAIKSPCQ 177
QY 194 SK-----DABYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS-PFG 238
DB 178 RETPEGAERKPWEPIYLGGVFQLEKGRDLSTEVNQPEYLDLAESQVYFG 228

RESULT 4
I54490
tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C:Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 04-Feb-2000
C:Accession: I54490
R:Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus le
A:Reference number: I54490; MUID:92218012; PMID:1348497
A:Accession: I54490
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: GB:M59233; NID:G202506; PIDN:AAA40596.1; PID:G202507
C:Genetics:
A:Gene: P1TNF
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 10.1%; Score 129.5; DB 2; Length 235;
Best Local Similarity 24.5%; Pred. No. 0.0012;
Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 79/1; 95/1
A;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxic; glycoprotein; lipoprotein; lymphokine; macrophage; me
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

Query Match 9.8%; Score 126; DB 1; Length 234;
Best Local Similarity 22.5%; Pred. No. 0.0023;
Matches 45; Conservative 35; Mismatches 72; Indels 48; Gaps 9;

QY 62 ISTVQEKQ-----QNTISPLVR-----ERGP-QRVAHITGTRGRSNTLSPNSKNEKALG 110
Db 56 IGPQREQLPNAFQSIPLAQLTRSSRTPSPDKPAHVVA-----NPQAEQ 101

QY 111 RKINSWESSRSGHSPFLSNLHNLGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQMVQ 170
Db 102 QL--QWLSGRANALLANGVLTNDQVLPDLGLIYSQVLPFGQ-----GCPSTH 150

QY 171 YIYKYT-----SYDPILLMKSAKNSKWSKDAEYG-----LYSIYQGGIFELKENDRIF 219
Db 151 VLLTHISRLAYSYPKSVNLLSAIKSPCHTESPEQAEKXPWEPIYLVGGVQLEKGDQLS 210

QY 220 VSTVNEHLIDMDHEAS-FFG 238
Db 211 AEINQPNYLDFAESGQVYFG 230

RESULT 7
OWHUN
tumor necrosis factor alpha precursor [validated] - human
N;Alternate names: cachectin; TNFA
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 08-Dec-2000
C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; B
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica,
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and ch
A;Reference number: A93585; MUID:86016093; PMID:2995927
A;Accession: A93585
A;Molecule type: DNA
A;Residues: 1-233 <NED>
A;Cross-references: GB:X02159; GB:X02159; NID:937209; PIDN:CAA26669.1; PID:937210
R;Iris F.J.M.; Bougueret, L.; Prieur, S.; Caterina, D.; Perrot, V.; Jur
Nature Genet. 3, 137-145, 1993
A;Title: Dense Ali clustering and a potential new member of the NFkappaB family within
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36153
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <TRI>
A;Cross-references: EMBL:Z15026; NID:937211; PIDN:CAA78745.1; PID:937212
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to
A;Reference number: A93351; MUID:85086244; PMID:6392892
A;Accession: A93351
A;Molecule type: mRNA
A;Residues: 1-233 <PEN>
A;Cross-references: GB:X02910; GB:X02910; NID:937209; PIDN:CAA26669.1; PID:937210
A;Note: this protein was isolated from the monocytic-like cell line HL-60 from a promye
R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.
Science 228, 149-154, 1985
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A;Reference number: A44189; MUID:85142190; PMID:3856324
A;Accession: A44189
A;Molecule type: mRNA
A;Residues: 1-62, 'S', 64-233 <WAN>

QY 72 ISPLVRGPORVAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSGH 123
Db 56 IGPQREKFPNNLP--IIGSNAQTLTRSSQNSGSDKFAVHVAHQVDEQLEWLSRGAN 113

QY 124 SFLSN-LHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQMVYIKY-TSYPDP 181
Db 114 ALLANGMDLKNQLVIPADGLYLVYSQVLPFGQ-----GCSYVLLTHTVSRFAVSIEDK 168

QY 182 ILLMKASNSKWSKDAEYG-----LYSIYQGGIFELKENDRIFVSTVNEHLIDMDHEAS 235
Db 169 VNLLSAIKSPC-PKETPSSELKPWVEPIYLVGGVQLEKGDRLSAEVLNPLPYLDFAESGQ 227

QY 236 -FFG 238
Db 228 VYFG 231

RESULT 5
S24641
lymphotoxin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C;Accession: I46046; S24641
R;Clutts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
A;Reference number: I46046; MUID:94083525; PMID:8260599
A;Accession: I46046
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-204 <CL2>
A;Cross-references: EMBL:Z14137; NID:9796; PIDN:CAA78510.1; PID:9797
C;Genetics:
A;Introns: 32/3; 68/1
A;Superfamily: tumor necrosis factor

Query Match 9.9%; Score 127.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. No. 0.0015;
Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 61 TISTVQEKQNTISPLVRGPORVAHITG-----TRGRSNTLSPNSKNEKALGRKI 113
Db 40 TPSAAQPAHQQL-PTPTFRGTGLKPAHLVGDPSQTQDSLWRANT-----DRAFLR-- 88

QY 114 NSWESSRSGHSPFLSNLHNLGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQMVYIY 173
Db 89 -----HGF-----SLSNLLVPTSLGIFYVSYQVPSGCGFPRAPTPLYLAHEVQ 135

QY 174 KYT-SYDPILLMKASNSKWSKDAEYGFIYYSQGGIFELKENDRIFVSTVNEHLIDMD 231
Db 136 LFSQPQYFFRVPLLSAQKSCVCPQGPW-VRSYVQGAFFLTRGDQLSTHTDGIHLL-LS 193

QY 232 HEASFFGAF 240
Db 194 PSSVFFGAF 202

RESULT 6
JQ1344
tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 04-Feb-2000
C;Accession: JQ1344
R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A;Reference number: JQ1344; MUID:92084125; PMID:1748301
A;Accession: JQ1344
A;Molecule type: DNA
A;Residues: 1-234 <SUX>
A;Cross-references: GB:M64087; NID:9164244; PIDN:AAA30959.1; PID:9164245

A:Cross-references: GB:M10988; NTD:g3397377; PIDN:AAA611598.1; PID:g339738
A:Rukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Ando, S.;
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A:Reference number: A61478; MUID:88301617; PMID:2841543
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102/109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180-181
A:Rarmenout, A.; Franssen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, M.
Eur. J. Biochem. 132, 515-522, 1985
A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A:Reference number: I53311; MUID:86030296; PMID:3932069
A:Accession: I53311
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <VAR>
A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A:Experimental source: U-937 cells
R:Takakura-Iamamoto, R.; Iamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967; PMID:8631363
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TAK>
R:D'Alfonso, S.; Ricciardi, P.M.
Immunogenetics 39, 150-154, 1994
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region
A:Reference number: I54522; MUID:94102809; PMID:7903959
A:Accession: I54522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <DAL>
A:Cross-references: GB:S68530; NID:G544751
R:Stevenson, P.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysines
A:Reference number: A59163; MUID:93018820; PMID:1402651
A:Contents: annotation; identification of myristylated lysines
R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bringmann, R.
J. Biol. Chem. 260, 2345-2354, 1985
A:Title: Human tumor necrosis factor. Production, purification, and characterization.
A:Reference number: A92511; MUID:85130974; PMID:3871770
A:Contents: annotation; disulfide bond
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
out detriment to normal cells. It can also act synergistically with interferon gamma to
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely
ut are produced by different cell types and have different induction kinetics.
C:Genetics:
A:Gene: GDB:TNF; TNFA
A:Cross-references: GDB:120441; OMIM:191160
A:Map position: 6p21.3-6p21.3
A:Introns: 62/3; 78/1; 94/1
C:Complex: homotrimer
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage
F:7-76/Domain: propeptide status predicted <PRO>
F:77-233/Product: tumor necrosis factor #status experimental <MAT>
F:19, 20/Binding site: myristate (lys) (covalent) #status experimental
F:81/Binding site: carboxylate (Ser) (covalent) (partial) #status experimental
F:145-177/Disulfide bonds: #status experimental
Query Match 9.6%; Score 123; DB 1; Length 233;
Best Local Similarity 23.0%; Pred. No. 0.0042;
Matches 43; Conservative 32; Mismatches 70; Indels 42; Gaps 8;
QY 80 GPOR-----VAAHITGRGSNTLSFNSK-----NEKALGRKINSSESSGH 123
DB 57 GPORPEPRLSLISPLAQAVRSSRT---PSDKPAHVAVNPAQEQGL--QWLNRANA 111
QY 124 SFTSNLHNLNGELVIHKGFIYISQTYFRQEEIKENTKNDKMWQIYKYT-----S 177
DB 112 LLANGVELRNQLVWPSEGVLIVYSQVLFKQ-----GCPSTHLVLTHTSRIVS 162

QY 178 YDPILLMKSNRNCSWK-----DAEVLGIYSIQGIFELKENDRIFFSVSTNEHLIDMDH 232
:
:
:
DB 163 YQTKNVLLSAIKSPCQRTEPGAENAKFPWFIYLGGVQLKEGRLSAEINRRPYDLDFAE 222
:
:
:
:

QY 233 EAS-PFG 238
:
:
DB 223 SGQVFYG 229

RESULT 8

QWFUX

Lymphotoxin alpha precursor - human

N;Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
S;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence revision 07-Jul-1995 #text change 16-Jun-2000
C;Accession: A92755; S36154; I54482; A93350; B32877; A91306; A61478; S26951; A.5.
R;Nedwin, G.B.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.

J. Cell. Biochem. 29, 171-181, 1985

A;Title: Structure and chromosomal localization of the human lymphotoxin gene.
A;Reference number: A92755; MUID:86086150; PMID:3001109
A;Accession: A92755

A:Molecule type: DNA
A;Residues: 1-59, 'N', 61-205 <NED>
R;Zis, F.J.M.; Bougudieret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot,
Nature Genet. 3, 137-145, 1993

A;Title: Dense Alu clustering and a potential new member of the NFkappaB family
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36154

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A;Residues: 1-12, 'R', 14-205 <IRI>
A;Cross-references: EMBL:D15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, August
R;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991

A;Title: Haplotypic polymorphisms of the TNFB gene.
A;Reference number: I54482; MUID:91139175; PMID:1671667
A;Accession: I54482

A>Status: translation not shown; translated from GB/EML/DDBJ

A:Molecule type: DNA
A;Residues: 1-124, 'P', 126-205 <RES>
A;Cross-references: GB:M55913; NID:g939742; PIDN:AAB59455.1; PID:g339743
A;Experimental source: ancestral haplotype 57.1
A;Note: 59-Asn was also found (ancestral haplotype 8.1)
R;Gray, P.W.; Agarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett,
Nature 312, 721-724, 1984

A;Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine w/o
A;Reference number: A93350; MUID:85086243; PMID:6334807
A;Accession: A93350

A:Molecule type: mRNA
A;Residues: 1-205 <GRA>
A;Cross-references: GB:X01393; NID:g34444; PIDN:CAA25649.1; PID:g34445
A;Experimental source: lymphoblastoid cell line RPMI-1788
R;Goedel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.B.; Pallada,
Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986

A;Title: Tumor necrosis factors: gene structure and biological activities.
A;Reference number: A32877; MUID:87217059; PMID:3472740
A;Accession: A32877

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A;Residues: 35-205 <GO>
R;Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
J. Biochem. 100, 727-733, 1986

A;Title: Cloning and expression of human lymphotoxin mRNA derived from a huma
A;Reference number: A91906; MUID:87057135; PMID:3536896
A;Accession: A91906

A:Molecule type: mRNA
A;Residues: 1-59, 'N', 61-205 <XOB>
A;Cross-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A;Note: The authors translated the codon TAT for residue 156 as Thr and ACC for
R;Fukuda, S.; Ando, S.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura,
Lymphoclin Res. 7, 175-185, 1988

QY 180 DPILLMKSARNCSWCKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE 233
Db 167 EKXNLLSAVKSPC-PKDTPEGAELKWPYEPYILGGVFLQEKGDQLSAEVNPVKYLDFAES 225
QY 234 AS-FFG 238
Db 226 GQVYFG 231

RESULT 10

tumor necrosis factor alpha precursor - rat
N/Alternate names: cachectin; TNF alpha
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text_change 04-Feb-2000
C/Accession: J00029; J00868; S21674
R/Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A/Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor alpha
A/Reference number: J00029
A/Accession: J00029
A/Molecule type: DNA
A/Residues: 1-235 <SHI>
R/Xwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A/Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A/Reference number: J00868; MUID:94040766; PMID:8224868
A/Accession: J00868
A/Molecule type: DNA
A/Residues: 1-235 <KWO>
A/Cross-references: GB:L00981; NID:9205253; PIDN:AAAL6275.1; PID:g205254
R/Sattler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A/Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro
A/Reference number: S21674; MUID:92329007; PMID:1627266
A/Accession: S21674
A/Molecule type: mRNA
A/Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>
A/Cross-references: GB:X68539; GB:S40199; NID:9395370; PIDN:CAA47146.1; PID:g395370
C/Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and
C/Genetics:
A/Gene: TNF-alpha
A/Intons: 62/3; 81/1; 97/1
C/Superfamily: tumor necrosis factor
C/Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane
F:80-235/Product: tumor necrosis factor #status predicted <Mat>
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (ser) (covalent) #status predicted
F:86/Binding site: carbohydrate (asn) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted

Query Match 9.4%; Score 121; DB 2; Length 235;
Best Local Similarity 23.0%; Pred. NO. 0.0063;
Matches 43; Conservative 35; Mismatches 79; Indels 30; Gaps 8;
QY 66 QEQQNISPVRGPRQVAHITGTRSNLTSSP-----NSRNEKALGRKINSWESS 119
Db 61 EEKFPNGPLI-----SSMAQTILTRSSQNSDKPVAHVANHQAEQL-----EWLSQ 110
QY 120 RSCHSFLNLHLENGELVTHEKGFYIYSCYTFRQEEIKENTKDKQVQIYKYT-SY 178
Db 111 RANALLANGVDKNDQNLVVPADGLYISQVLPKQG-----GCPDYVLLTHTVSRFAISY 165
QY 179 PDPILLMKSARNCSWCKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDH 232
Db 166 QEKVSLLSAISKSPC-PKDTPEGAELKWPYEPYILGGVFLQEKGDLLSAEVNPKYLDITE 224
QY 233 EAS-FFG 238
Db 225 SGQVYFG 231

RESULT 11

S22052
tumor necrosis factor alpha precursor - baboon
C/Species: Papio sp. (baboon)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
C/Accession: S22052
R/Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A/Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A/Reference number: S22052
A/Accession: S22052
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-233 <SAN>
A/Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160
C/Genetics:
A/Intons: 62/3; 78/1; 94/1
C/Superfamily: tumor necrosis factor
C/Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted
Query Match 9.3%; Score 120; DB 1; Length 233;
Best Local Similarity 23.0%; Pred. NO. 0.0076;
Matches 43; Conservative 32; Mismatches 70; Indels 42; Gaps 8;
QY 80 GPQR-----VAAHITGTRGRSNTLSSPNSK-----NEKALGRKINSWESSRSGH 123
Db 57 GPQREPPKDPSSLISLAQAVRSSRT---PSDKPVHVAVNPQASQL--QWLNRRANA 111
QY 124 SFLSNLHLENGELVTHEKGFYIYSCYTFRQEEIKENTKDKQVQIYKYT-----S 177
Db 112 LLANGVELRDNQNLVVPSEGLYISQVLPKQG-----GCPSTHVLTTHTISRIVS 162
QY 178 YPDPILLMKSARNCSWCK-----DASYGLYISYQGGIFELKENDRIFVSVTNEHLIDMDH 232
Db 163 YQTKVNLSSAISKSPCQRETPEGAEPWYEPYILGGVFLQEKGDRLSAEINLPYLDFAE 222
QY 233 EAS-FFG 238
Db 223 SGQVYFG 229
RESULT 12
JH0529
tumor necrosis factor alpha precursor - sheep
N/Alternate names: cachectin; TNF alpha
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
C/Accession: JH0529; S48118; S13114; S20661
R/Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A/Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with
A/Reference number: JH0529; MUID:92112044; PMID:1765267
A/Accession: JH0529
A/Molecule type: mRNA
A/Residues: 1-234 <GRE>
A/Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
A/Experimental source: alveolar macrophage
R/Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A/Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A/Reference number: S48118; MUID:92155784; PMID:1786996
A/Accession: S48118
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-234 <NMS>
A/Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R/Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A/Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A/Reference number: S13114; MUID:91067496; PMID:2251151
A/Accession: S13114

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62,64-234 <YOU>
A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A;Note: comparison with the introns of homologous sequences suggest that this is probably
C;Superfamily: tumor necrosis factor
C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;20/Binding site: myristate (Iys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

Query Match 9.1%; Score 117.5; DB 1; Length 234;
Best Local Similarity 23.0%; Pred. No. 0.013;
Matches 42; Conservative 30; Mismatches 78; Indels 33; Gaps 7;

Qy 80 GPOKVAHHITG---TRGRSNTL-SSPNKNEKALGRKINS-----WESSRSGHSFLS 127
Db 57 GPQREOSGAPGPNRPLVQTLSSSQASNNKPVAVHVNISAPGQLRWGDSVANALMAN 116
Qy 128 NLHNRNGELVTHEKGFYIYSQVYFRPQEEIKENTKNDKQMVYIYKYT-----SYPPD 181
Db 117 GVLEKDNQLVPTDGLYIYSQVLF-----GHGCPSTPLFLTHITISRIAVSYQTK 167
Qy 182 ILLMKARNCSWK-----DAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235
Db 168 VNILSAIKSPCHRETLGSAKAPWPEIYOGGVFQLEKGRDLRAEINLPYLDYAESGV 227
Qy 236 FFG 238
Db 228 YFG 230

RESULT 13
S06192
tumor necrosis factor alpha precursor - goat (fragment)
N;Alternate names: cachectin; TNF alpha
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-2000
C;Accession: S06192; S41867
R;Goldstein, I.M.; Henner, D.; Talhouk, A.
submitted to the EMBL Data Library, March 1989
A;Reference number: S06192
A;Accession: S06192
A;Molecule type: mRNA
A;Residues: 1-193 <GOL>
A;Cross-references: EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993
R;Rinestad, E.
submitted to the EMBL Data Library, January 1994
A;Reference number: S41867
A;Accession: S41867
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 35-38,'S',40-78,'A',80-88,'N',90-114,'O',116-123,'D',125-144,'G',145-173,'L'
A;Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein
F;42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;106-138/Disulfide bonds: #status predicted

Query Match 9.0%; Score 115.5; DB 2; Length 193;
Best Local Similarity 20.4%; Pred. No. 0.014;
Matches 45; Conservative 36; Mismatches 79; Indels 61; Gaps 9;

Qy 29 FNDEESMNSPCQVQKWLQRLVRLMILFTSBETISTYQEKQNTSPLVRERGPGQVAHI 88
Db 19 PEEQSPAGPSFN-----RPLVQ--TLRSSSQASS-----NKPVAHV 53
Qy 89 TGTGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFLSNLHNRNGELVTHEKGFYIYS 148
Db 54 VA-----NISAPGQLR-----WGDSYANALKANGVELKDNQLVPTDGLYIYS 97

Qy 149 QTYRFOEETKENTKNDKQMVYIYKYT-----SYDPILLMKARNCSWK-----DAE 198
Db 98 QVLFER-----GHGCPSTPLFLTHITISRIAVSYQTKVNILSAIKSPCHRETPAEAK 148
Qy 199 YGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
Db 149 PWPEIYOGGVFQLEKGRDLRAEINQPEYLDYAESGGQVYFG 189

RESULT 14
B27303
tumor necrosis factor beta precursor - mouse
N;Alternate names: lymphotoxin; TNF beta
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: B27303; S01342; S10083; I56004; I48853; I55980
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor n
A;Reference number: A33679; MUID:88067722; PMID:3684584
A;Accession: B27303
A;Molecule type: DNA
A;Residues: 1-202 <SEM>
A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68529.1; PID:g54831
R;Nedospasov, S.A.; Hirt, B.; Shakhov, A.N.; Dobrynin, V.N.; Kawashima, E.; Accolla, R
Nucleic Acids Res. 14, 7713-7725, 1986
A;Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) ar
A;Reference number: S01342; MUID:87040736; PMID:3490653
A;Accession: S01342
A;Molecule type: DNA
A;Residues: 1-11,139-160,'CG',163-178 <NED>
A;Cross-references: EMBL:X06217
R;Weil, D.; Dautry, F.
Oncogene Res. 3, 409-414, 1988
A;Title: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA
A;Reference number: S10083; MUID:89144562; PMID:3147435
A;Accession: S10083
A;Molecule type: mRNA
A;Residues: 6-202 <WEI>
A;Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; PID:g736269
R;Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D.
J. Immunol. 139, 476-483, 1987
A;Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the clone
A;Reference number: I56004; MUID:87252204; PMID:2885372
A;Accession: I56004
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-25,'P',27-202 <REG>
A;Cross-references: GB:M17015; NID:gl98880; PIDN:AAA39450.1; PID:g387407
R;Gray, F.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddle, N.
Nucleic Acids Res. 15, 3937, 1987
A;Title: The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.
A;Reference number: I48853; MUID:87231097; PMID:3588316
A;Accession: I48853
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-202 <RE2>
A;Cross-references: EMBL:Y00137; NID:g54842; PIDN:CAA68330.1; PID:g54843
R;Li, C.
J. Immunol. 138, 4496-4501, 1987
A;Title: Cloning and expression of murine lymphotoxin cDNA.
A;Reference number: I55980; MUID:87224127; PMID:2884262
A;Accession: I55980
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-202 <RES>
A;Cross-references: GB:M16819; NID:g202088; PIDN:AAA40460.1; PID:g202089
C;Comment: The first intron occurs in the 5'-untranslated region.
C;Genetics:
A;Gene: Tnfrb
A;Map position: 17
A;Introns: 32/3; 66/1

C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

Query Match 8.9%; Score 114; DB 1; Length 202;
Best Local Similarity 23.5%; Pred. No. 0.02;
Matches 38; Conservative 25; Mismatches 81; Indels 18; Gaps 3;

QY 80 GPCRVAHHITGRGRSNTLSSPNSKNEKALGRKINSWSSRGSHGFLSNHLRNGELVIH 139
 : : : : : : : :
Db 56 GILKPAALHGVPSKQNSL-----LWRASDTEALRHGFLSNNSLLIP 99

QY 140 EKGFFYYISQYTFPQBEIKENTKNDQMQVYIKYTS-YPDILLMSKARNSCWSKDAE 198
 : : : : : : : :
Db 100 TSLGFLFYVQVVFEGSCSPRAIPTIYLAHEVQLFSSQYPPHVPULL-SAQKSVYFGLQG 158

QY 199 YGLYSIYQCGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 : : : : : : : :
Db 159 PWRVSMYOGAVFLSKGDSLSTHDGISHLHFSPSSVFFGAF 200
 : : : : : : : :

RESULT 15

S52715 tumor necrosis factor alpha precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C:Accession: S52715
R:Verteats, B.; Gaidulis, L.
submitted to the EMBL Data Library, March 1995
A:Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and bo
A:Reference number: S52715
A:Accession: S52715
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-185 <EMBL>
A:Cross-references: EMBL:Z4808; NID:g755701; PIDN:CAA89743.1; PID:g755702
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein
F:33/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:97-129/Disulfide bonds: #status predicted

Query Match	8.8%;	Score 113.5;	DB 2;	Length 185;
Best Local Similarity	25.0%;	Pred. No. 0.02;		
Matches	45;	Conservative	29;	Mismatches 79;
			Indels	27;
			Gaps	9;

QY	80	GPORVA	HHITG	REGRS	---	NTL	-SSP	SKNE	KALGR	---	KINS	----	WESS	RSCH	SFLS	127	
																:	
Db	8	GPOR	EQSG	PGGS	INS	PLVQ	LRSS	QAS	SNKPV	AAHV	ADINS	PGOL	RW	MSDY	ANAL	MAN 67	
																:	
QY	128	NH	L	ANGEL	VI	THE	K	GFY	YI	YQ	TFR	Q	EE	I	KENT	KDKQ	MYIYK -YTSY
Db	68	GK	LEDN	QL	W	P	ADG	L	YI	Y	Q	V	L	F	R	GQ	----
QY	186	K	ARN	S	C	-----	W	S	K	D	A	E	G	L	I	Y	G
Db	123	S	A	I	K	P	H	R	E	T	P	E	W	A	-E	A	K

Search completed: June 3, 2004, 09:04:57
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:57:01 ; Search time 17 Seconds
(without alignments)
744.297 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287

Sequence: 1 INELKQMDKYSGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 56376

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	12.4	174	TN15 HUMAN	Q91510 homo sapien
2	159.5	12.4	240	TN14 HUMAN	Q43557 homo sapien
3	152.5	11.8	239	TN14 MOUSE	Q9qy9 mus musculus
4	136.5	10.6	235	TNFB RABIT	P04924 cryctolagus
5	134.5	10.5	204	TNFB PIG	P26445 sus scrofa
6	132.5	10.3	234	TNFA CAVPO	P51435 cavia porce
7	130	10.1	232	TNFA PIG	P23563 sus scrofa
8	129.5	10.1	235	TNFA PERLE	P36939 peromyscus
9	127.5	9.9	234	TNFB BOVIN	Q06600 bos taurus
10	126	9.8	234	TNFA HORSE	P29553 equus caball
11	125	9.7	233	TNFA MARMO	Q35734 marmota mon
12	123	9.6	233	TNFA HUMAN	P01375 homo sapien
13	122.5	9.5	229	TNFA CEREL	P51743 cervus elap
14	122	9.5	205	TNFB HUMAN	P01374 homo sapien
15	122	9.5	232	TNFA PANTR	Q8had9 pan troglod
16	121	9.4	235	TNFA MOUSE	P06804 mus musculus
17	121	9.4	235	TNFA RAT	P16599 rattus norv
18	120	9.3	205	TNFB MARMO	Q9jmd9 marmota mon
19	120	9.3	233	TNFA PAPSP	P33620 papio sp. (
20	118	9.2	233	TNFA TURTR	Q9bea1 tursiops tr
21	117.5	9.1	201	TNFB MACEU	Q9xt48 macropus eu
22	117.5	9.1	234	TNFA SHEEP	P23383 ovis aries
23	117	9.1	233	TNFA MACMU	P48094 macaca mula
24	117	9.1	233	TNFA PAHU	Q77510 papio hamad
25	116.5	9.1	233	TNFA CANFA	P51742 canis faml
26	116	9.0	233	TNFA MACFA	P79337 macaca fasc
27	116	9.0	233	TNFA SAISC	Q8mk98 salmirl sci
28	114	8.9	202	TNFB MOUSE	P09425 mus musculus
29	113.5	8.8	233	TNFA TRIVU	P79374 trichosurus
30	113.5	8.8	234	TNFA BOSIN	P59684 bos indicus
31	113	8.8	233	TNFA BOVIN	Q06299 bos taurus
32	113	8.8	233	TNFA BUBBU	P59693 bubalus bub
33	113	8.8	233	TNFA LAMGL	P59694 lama glama

ALIGNMENTS

RESULT 1

ID	TN15 HUMAN	STANDARD;	PRT;	174 AA.
AC	O91510;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).			
GN	TNFSF15 OR VEGI OR TLI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Umbilical vein;			
RC	MEDLINE=99091541; PubMed=9872942;			
EA	Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,			
EA	Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,			
EA	Li L.-F., Gentz R., Yu G.-L.,			
RT	"VEGI, a novel cytokine of the tumor necrosis factor family, is an angiogenesis inhibitor that suppresses the growth of colon carcinomas in vivo."			
RL	FASEB J. 13:181-189(1999).			
CC	- FUNCTION: Inhibits vascular endothelial growth and angiogenesis (in vitro).			
CC	- SUBUNIT: Homotrimer (Potential).			
CC	- SUBCELLULAR LOCATION: Type II membrane protein (Probable).			
CC	- TISSUE SPECIFICITY: Specifically expressed in endothelial cells. Detected in placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.			
CC	- SIMILARITY: Belongs to the tumor necrosis factor family.			
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CC	EMBL; AF039330; AAD08783.1; -.			
DR	HSSP; P50591; 1DQ0.			
DR	Genem; HGNC:11931; TNFSF15.			
DR	MIM; 604052; -.			
DR	GO; GO:0005887; C: integral to plasma membrane; TAS.			
DR	GO; GO:0005102; F: receptor binding; TAS.			
DR	GO; GO:0000004; P: regulation of cell cycle; TAS.			
DR	InterPro; IPR006053; TNF_abs.			
DR	InterPro; IPR006052; TNF_family.			
DR	InterPro; IPR008983; TNF_like.			
DR	InterPro; IPR003636; TNF_subf.			
DR	Pfam; PF00229; TNF; 1.			
DR	PRINTS; PR01234; TNFCROSISFCT.			
DR	Prodom; PD002012; TNF_subf; 1.			

34	112.5	8.7	234	1	TNFA_CAPHI	P13296 capra hircu
35	112	8.7	233	1	TNFA_DELLE	Q8wnr1 delphinapte
36	111.5	8.7	202	1	TNFB_RAT	Q06332 rattus norv
37	111	8.6	240	1	TNFS_MACNE	Q9bom7 macaca neme
38	110	8.5	233	1	TNFA_PAPAN	P59695 papio anubi
39	108	8.4	233	1	TNFA_MACEU	O77764 macropus eu
40	107	8.3	197	1	TNFB_RABIT	P10154 oryctolagus
41	106.5	8.3	150	1	TNFC_PIG	Q9tbv8 sus scrofa
42	104.5	8.1	233	1	TNFA_FELCA	P19101 felis silve
43	77.5	6.0	229	1	CEMA_ARATH	P56783 arabidopsis
44	75.5	5.9	142	1	DKSA_CAUCR	Q32347 caulobacter
45	73.5	5.7	206	1	KGUA_LACPL	Q88w17 lactobacill

DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF 2; 1.
KW Cytokine; Transmembrane; Glycoprotein; signal-anchor.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
FT DISULFID 85 125 POTENTIAL.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 174 AA; 20131 MW; CCB83BA7E673B98 CRC64;
Query Match 12.4%; Score 160; DB 1; Length 174;
Best Local Similarity 35.3%; Pred. No. 2.5e-06;
Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8;
QY 116 WSSRSCHGFLGN-LHLRNGELVIEHKGFIYYSQTYPRFO-----EIKENTKDK--QM 168
DB 42 WE-HELGLAFTKRMVNTYKFLIPESGDYFIYSQVTRFGMTSECEIRQAGRPKPDSI 100
QY 169 VQYIYKYT-SYDPILLMKASRNSCWSDAEVG---LYSIYGGIFELKENDRIPVSVTN 224
DB 101 TVVITKVTDSYEPETQLLMTKTSVC-----EVGSNWFQIYLGAMFSLQEGDKLMVNVSD 155
QY 225 EHLIDMDHE-AGFFGAFLV 242
DB 156 ISLVDYTKEDKTFYFGALL 174
RESULT 2
TN14_HUMAN STANDARD; PRT; 240 AA.
ID TN14_HUMAN Q9WVF8; Q96LD2;
AC Q43557; Q75476; Q9WVF8; Q96LD2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
mediator-ligand) (HVEM-L).
GN TNFSF14 OR LIGHT OR HVEM-L.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98122340; PubMed=9462508;
RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
RA Ware C.F.;
RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
RT ligands for herpesvirus entry mediator.";
RL Immunity 8:21-30(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=9438532; PubMed=9765287;
RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
RA Tan K.B., Dede K., Spanapanato J., Silverman C., Hensley P.,
RA Diprinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
RA Truneh A., Young P.R.;
RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
RT HVEM/FR2, stimulates proliferation of T cells and inhibits HT29 cell
RT growth.";
RL J. Biol. Chem. 273:27548-27556(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
RX MEDLINE=21528948; PubMed=11673523;
RA Granger S.W., Butrovich K.D., Houshand P., Edwards W.R., Ware C.F.;
RT "Genomic characterization of LIGHT reveals linkage to an immune
RT response locus on chromosome 19p13.3 and distinct isoforms generated
RT by alternate splicing or proteolysis.";
RL J. Immunol. 167:5122-5128(2001).
RN [4]

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Phaley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gricham J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
CC decoy receptor TNFRSF6B modulates its effects. Activates NFkB,
CC stimulates the proliferation of T cells, and inhibits growth of
CC the adenocarcinoma Ht-29. Acts as a receptor for Herpes simplex
CC virus.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC (isoform 1); Cytoplasmic (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O43557-1; Sequence=Displayed;
CC Name=2; Synonyms=LIGHT delta-TM;
CC IsoId=O43557-2; Sequence=VSP_006452;
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
CC FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
CC NONHEMATOPOIETIC TUMOR LINES.
CC -!- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
CC -!- PTM: N-glycosylated.
CC -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 178.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF036581; AAC39563.1; -
CC EMBL; AF064090; AAC25169.1; -
CC EMBL; AY028261; AAK36160.1; -
CC EMBL; BC018058; AAH18058.1; ALT_FRAME.
CC HSP; P01375; 4TSV.
CC Genew; HGNC:11930; TNFSF14.
CC MIM; 604520; -
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0006917; P:induction of apoptosis; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF-like.
CC InterPro; IPR003636; TNF_subf.
CC Fram; PF00229; TNF; 1.

TNFA_RABIT
 ID TNFA_RABIT STANDARD; PRT; 235 AA.
 AC P04924.
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (TNF-a) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91065534; PubMed=2249779;
 RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
 RA Nedospasov S.A.;
 RT "Structural analysis of the rabbit TNF locus, containing the genes
 RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
 RT factor).";
 RL Gene 95:215-221(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86219712; PubMed=3519138;
 RA Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
 RA Wallace R.B.;
 RT "Molecular cloning of the gene encoding rabbit tumor necrosis
 RT factor.";
 RL DNA 5:157-165(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86219711; PubMed=3519137;
 RA Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
 RA Hayashi H., Kato M., Seko M.;
 RT "Molecular cloning and expression in Escherichia coli of the cDNA
 RT coding for rabbit tumor necrosis factor.";
 RL DNA 5:149-156(1986).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
 CC cancer and infection, and is characterized by general ill health
 CC and malnutrition.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M12845; AAA31486.1; -;
 CC EMBL; M12846; AAA31482.1; -;
 CC EMBL; M60340; AAA31484.1; -;
 CC PIR; A25454; A25451.
 CC HSP; P06804; 2TNF.
 DR InterPro; IPR006053; TNF_abc.

DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECOSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS00049; TNF 2; 1.
 DR Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
 KW TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 1 235
 FT TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT CHAIN 80 235
 FT CYTOPLASMIC (POTENTIAL)
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT TRANSMEM 36 56
 FT (POTENTIAL).
 FT DOMAIN 57 235
 FT EXTRACELLULAR (POTENTIAL).
 FT SITE 79 80
 FT CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD_RES 2 2
 FT PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 148 179
 FT BY SIMILARITY.
 FT CONFLICT 63
 FT MISSING (IN REF. 3).
 SQ SEQUENCE 235 AA; 25816 MW; 61017D0BD2EF871 CRC64;
 Query Match 10.6%; Score 136.5; DB 1; Length 235;
 Best Local Similarity 23.0%; Pred. No. 0.00032;
 Matches 42; Conservative 37; Mismatches 81; Indels 23; Gaps 7;
 QY 72 ISPLVERGPQVAHITGRGNTL--SSPNSKNEKALGRKINS-----WESSRG 122
 DB 56 IGQEEQEPNNL--HLNVPVQMVTLRASALSRLDKPLAHVAVNPGVQLWLSQAN 113
 QY 123 HSFLSNLHRLNGELVIHERGFYIYSQTYFRFQEEIKENTKNDKQMVQYIKY-TSYDDP 181
 DB 114 ALLANGKLTNDQLVVPADGLYLYSQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNK 168
 QY 182 ILLMKASRNSCWSKDAEYG-----LVSIVQGGIFELKENDRIFSVTNEHLIDMDHEAS- 235
 DB 169 VNLSLAIKSPCHRETPPEEAFPMWYEPYILGVGVFQLEKGRDUSTEVNQPEYLDLAESGV 228
 QY 236 FFG 238
 DB 229 YFG 231
 RESULT 5
 TNFB_PIG
 ID TNFB_PIG STANDARD; PRT; 204 AA.
 AC P26445.
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lymphotoxin-alpha precursor (lr-alpha) (TNF-beta) (Tumor necrosis
 DE factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91340150; PubMed=1874444;
 RA Kubert P., Wuehrich C., Peterhans E., Pauli U.;
 RT "The porcine tumor necrosis factor-encoding genes: sequence and
 RT comparative analysis.";
 RL Gene 102:171-178(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Large white; TISSUE=Fibroblast;
 RX MEDLINE=21108615; PubMed=11169259;
 RA Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
 RA Renard C.;
 RT "Sequence of the swine major histocompatibility complex region
 RT containing all non-classical class I genes.";

```

RL Tissue Antigens 57:55-65(2001).
CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
CC heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC produced by lymphocytes and cytotoxic for a wide range of tumor
CC cells in vitro and in vivo.
CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC associated (heterotrimers) (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X54859; CRA38638.1; -.
CC EMBL; AJ251914; CAB63853.1; -.
CC PIR; S17289; S17289.
CC HSSP; P01374; 1TNR.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS0049; TNF_2; 1.
CC Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 33
FT CHAIN 34 204 LYMPHOTOXIN-ALPHA.
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 204 AA; 21960 MW; 81263187435556AC CRC64;

Query Match 10.5%; Score 134.5; DB 1; Length 204;
Best Local Similarity 24.7%; Pred. No. 0.00039;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;

QY 63 STVQKQNIQPLVREGRQVAAHITG-----TGRSNTLSPPNSKNEKALGRKINS 115
DB 42 SAAQPAHQH-PPKHARGLTLPAAHLVGDPTPDSLRWANT-----DRAFLR---- 88

QY 116 WESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKY 175
DB 89 -----HGFL-----LSNNLLIVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF 137

QY 176 TS-YDPILLMKARSNCWSKDAEYGLYSIVGGGIFELKENDRIFVSVTNEHLTMDHEA 234
DB 138 SQYFFHVLISQAQSVCPGPGPW-VRSVYQGVAFLLTQGDQLSTHTDGTPHLLSPSS 196

QY 235 SFFGAF 240
DB 197 VFFGAF 202

RESULT 6
TNFA_CAVPO STANDARD; PRT; 234 AA.
AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
GN TNF OR TNFSF2 OR TNFA.
OS Cavia porcellus (Guinea pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RT Juan H.T., Kelly F.J., Single C.D.;
RT "Cloning and characterization of guinea pig TNF-alpha cDNA.";
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=Dunkin-Hartley;
RC MEDLINE=97462215; PubMed=9316485;
RX White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U39839; AAB06492.1; -.
CC EMBL; U77036; AAB19210.1; -.
CC HSSP; P06804; 2TNF.
CC InterPro; IPR006053; TNF_abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS0049; TNF_2; 1.
CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 80 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 147 178 BY SIMILARITY.
SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 10.3%; Score 132.5; DB 1; Length 234;
Best Local Similarity 24.6%; Pred. No. 0.00068;

```

Matches 44; Conservative 33; Mismatches 77; Indels 25; Gaps 7;
 QY 80 GPQRVAAHITGT--RGRSNTL---SSPNSKNEKALGRKINS-----WESSRSGHSFL 126
 DB 57 GQREEQFGPPFPPLAQLTLRSGASQNDNDKPKVAHVANQAAEEQLWLSKRANALLA 116
 QY 127 SNLHLRNGELVHEKGFYIYQTYFRQBEIEKENTKNDKQWQVIYKY-TSYDDPILLM 185
 DB 117 NGMGLSDNQLVVPFSDGLYLIYSQVLFKGO-----GCPSYLLLTHTVSVLAVSYPEKVNLL 171
 QY 186 KGRASCMWKADEYG-----LXSYQGGIFELKENDRIFVSVTNEHLIDM-DHEASPPG 238
 DB 172 SAIKSPCKETPEGAERKPWEPIYLGQVFLQKGRDLSEAVNLPOYLDFAADSGQIYFG 230

RESULT 7
 TNFA_PIG STANDARD; PRT; 232 AA.
 AC P23563;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (TNF-a) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CX NCB_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=91016861; PubMed=2216741;
 RA Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;
 RT "Gene sequence of porcine tumor necrosis factor alpha.";
 RL Nucleic Acids Res. 18:5564-5564 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=91340150; PubMed=1874444;
 RA Kuhnert P., Wuehrich C., Peterhans E., Pauli U.;
 RT "The porcine tumor necrosis factor-encoding genes: sequence and
 comparative analysis.";
 RL Gene 102:171-178 (1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Macrophage;
 RA Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;
 RT "Complete nucleotide sequence of a cDNA encoding porcine tumor
 necrosis factor-alpha.";
 RL Anim. Biotechnol. 2:97-105 (1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Large white; TISSUE=Fibroblast;
 RX MEDLINE=21108615; PubMed=11169259;
 RA Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
 RA Renard C.;
 RT "Sequence of the swine major histocompatibility complex region
 containing all non-classical class I genes.";
 RL Tissue Antigens 57:55-65 (2001).
 RN [5]
 RP SEQUENCE OF 44-232 FROM N.A.
 RX MEDLINE=90034181; PubMed=2478420;
 RA Pauli U., Beutler B., Peterhans E.;
 RT "Porcine tumor necrosis factor alpha: cloning with the polymerase
 chain reaction and determination of the nucleotide sequence.";
 RL Gene 81:185-191 (1989).
 CC -/- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
 induce cell death of certain tumor cell lines. It is potent
 pyrogen causing fever by direct action or by stimulation of
 interleukin 1 secretion and is implicated in the induction of
 cachexia. Under certain conditions it can stimulate cell
 proliferation and induce cell differentiation.

CC -/- SUBUNIT: Homotrimer (By similarity).
 CC -/- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 extracellular soluble form (By similarity).
 CC -/- PTM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -/- PTM: The membrane form, but not the soluble form, is
 phosphorylated on serine residues. Dephosphorylation of the
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 similarity).
 CC -/- DISEASE: Cachexia accompanies a variety of diseases, including
 cancer and infection, and is characterized by general ill health
 and malnutrition.
 CC -/- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X54001; CAA37949.1; -;
 DR EMBL; X54859; CAA38639.1; -;
 DR EMBL; X57321; CAA40591.1; -;
 DR EMBL; AJ251914; CAB63852.1; -;
 DR EMBL; M29079; AAA31128.1; -;
 DR PUR; S12606; S12606.5;
 DR HSP; P01375; 4TSV.
 DR InterPro; IPR006053; TNF_abs.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
 FT CHAIN 1 232 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT DOMAIN 77 232 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT TRANSMEM 36 56 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 57 232 EXTRACELLULAR (POTENTIAL).
 FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 144 176 BY SIMILARITY.
 SQ SEQUENCE 232 AA; 25254 MW; 65B28F702D99C8BE CRC64;
 Query Match 10.1%; Score 130; DB 1; Length 232;
 Best Local Similarity 25.1%; Pred. No. 0.0011;
 Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;
 QY 80 GPQRVAAHITGTGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHRNGEL 136
 DB 66 GPLSINFLAQLASSSQTSDKPAHVAVNVAKESQL--QWQGYANALLANGLKDNQL 123
 QY 137 VIHEKGFYIYQTYFRQBEIEKEN---TKNDKQWQVIYKYTSYDDPILMKASRNSCW 193
 DB 124 WPTDGLYLIYSQVLFKGOCPSTNVLHTTISRIA-----VSYQTKNLLSAIKSPCQ 177
 QY 194 SK-----DAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDEAS-PPG 238
 DB 178 RETPEGAERKPWEPIYLGQVFLQKGRDLSEAVNLPOYLDFAESQVYFG 228
 RESULT 8
 TNFA_PERLE
 ID TNFA_PERLE STANDARD; PRT; 235 AA.
 AC P36939;
 DT 01-JUN-1994 (Rel. 29, Created)

01-JUN-1994 (Rel. 29, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (TNF-a) (Cachectin).
 TNF OR TNFSF2 OR TNFA.
 Peromyscus leucopus (White-footed mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 Peromyscus.
 NCBI_TaxID=10041;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=92218012; PubMed=1348497;
 Crew M.D., Filipowicz M.E.;
 "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
 Peromyscus leucopus (family Cricetidae).";
 Immunogenetics 35:351-353(1992).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 induce cell death of certain tumor cell lines. It is potent
 pyrogen causing fever by direct action or by stimulation of
 interleukin 1 secretion and is implicated in the induction of
 cachexia. Under certain conditions it can stimulate cell
 proliferation and induce cell differentiation.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 extracellular soluble form (By similarity).
 CC -!- PM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -!- PM: The membrane form, but not the soluble form, is
 phosphorylated on serine residues. Dephosphorylation of the
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 similarity).
 CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
 cancer and infection, and is characterized by general ill health
 and malnutrition.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 EMBL; M59233; AAA40596.1; --
 PIR; I54490; I54490.
 HSP; P06804; 2TNF.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF_1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00649; TNF_2; 1.
 KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
 FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).
 FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 148 179 BY SIMILARITY.
 FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 235 AA; 25822 MW; 235ASCFC9F9AC624 CRC64;

Query Match 10.1%; Score 129.5; DB 1; Length 235;

Best Local Similarity 24.5%; Pred. No. 0.0012;
 Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;
 QY 72 ISPLVREGQQRVAHITGTGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSQH 123
 DB 56 IGPOREKFPNNLP--IIGSMAQTLTRSSSQNSDKPVAHVAVHNVQDQLEWLSGAN 113
 QY 124 SFLSN-LHLRNGELVIEHGPFYIYQTYFRQBEIKENTKNDKQMYOYIKY-TSYDDP 181
 DB 114 ALLANGMDLQNLVDPADGLVYVSVQVLFKQ-----GCSSYVLLTHTVSRAVSYEDK 168
 QY 182 ILLMKSARNSCWSKDAEYV-----LYSIYOGGFFELKENDRIFVSVTNEHLIMDHEAS 235
 DB 169 VNLISAIRKSPC-PRKTEPGESELKWPYEFYLGGVFQLEKGRDLSEVNLFXYLDFAESGQ 227
 QY 236 -FFG 238
 DB 228 VYFG 231
 RESULT 9
 TNFB BOVIN
 ID TNFB BOVIN STANDARD; PRT; 204 AA.
 AC Q06600;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
 factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94083525; PubMed=8260599;
 RA Cludes I., Cluter Y., Kettmann R., Burny A., Droogmans L.;
 "Cloning and characterization of the tandemly arranged bovine
 Lymphotoxin and tumour necrosis factor-alpha genes.";
 RT Lymphotoxin and tumour necrosis factor-alpha genes.
 RL Cytokine 5:338-341(1993).
 CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
 TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
 heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
 produced by lymphocytes and cytotoxic for a wide range of tumor
 cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
 LTA subunits or (less prevalent) two LTA and one LTB subunits (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
 associated (heterotrimers) (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 EMBL; Z14137; CAAT78510.1; --
 PIR; I46046; S24641.
 DR HSP; P01374; 1TNR.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF_1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.

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DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS0049; TNF 2; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 33 LYMFOXIN-ALPHA.
FT CHAIN 34 204 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 95 95
SQ SEQUENCE 204 AA; 22098 MW; 52A9F0A2CEDB5425 CRC64;

Query Match 9.9%; Score 127.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. No. 0.0015;
Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 61 TISTVQEQKQMSILVBERGQORVAHITG-----TRGSNTLSPNKNKALGRKI 113
DB 40 TPSAAQPAHQQL-PTPFRGTGLKFAAHLVGPSTQDSLWRANT-----DRAFLR-- 88
QY 114 NSWESSRSGHGSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIY 173
DB 89 -----HGF-----SLSNLSLVPTSLGLYFVVSQVFSGRGCFPRATPTPLVLAHEVQ 135
QY 174 KYT-SYDPDILMKSRNSCKDAEYGLIYIYQGGIFELKENDRIFVSVTN-EHLIDMD 231
DB 136 LFSQYPPHVELLSAQSKVCPQGPQPM-VRSVYQGAPELLTRGQDLSHTDGTSHLL-LS 193
QY 232 HEASPFQAF 240
DB 194 PSSVFFGAP 202

RESULT 10
ID TNFA_HORSE STANDARD; PRT; 234 AA.
AC P29553; Q9PTJ3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=92084125; PubMed=1748301;
RX Su X., Morris D.D., McGraw R.A.;
RA "Cloning and characterization of gene TNF alpha encoding equine tumor
RT necrosis factor alpha.";
RL Gene 107:319-321(1991).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Thoroughbred; TISSUE=Artery;
RA Ishida N., Sato F., Hasegawa T.;
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M64087; AAA30959.1; -.
DR EMBL; AB035735; BAA88349.1; -.
DR PIR; J01344; J01344.
DR HSP; P01375; IABM.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS0049; TNF 2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 78 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 146 178 BY SIMILARITY.
FT CONFLICT 177 179 PCH -> LAN (IN REF. 2).
SQ SEQUENCE 234 AA; 25469 MW; E79ACE91143DF373 CRC64;

Query Match 9.8%; Score 126; DB 1; Length 234;
Best Local Similarity 22.5%; Pred. No. 0.0023;
Matches 45; Conservative 35; Mismatches 72; Indels 48; Gaps 9;

QY 62 ISTVQEQK-----QNTISPLVR-----ERGF-QRVAHITGTRGNTLSPNKNKALG 110
DB 56 IGPQREQLPNFQSNPLAQLTSSSRTPSDKPAHVVA-----NPAERG 101
QY 111 RKINSWESSRSGHGSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQ 170
DB 102 QL--QWLGRANALLANGVKLTQNVLPDGLIYIYQVLFKQ-----GCPSTH 150
QY 171 YIVKYT-----SYDPDILMKSRNSCKDAEYG-----LYSIYQGGIFELKENDRIF 219
DB 151 VILTHITSLAVSYPSKVNLSAISKPSCHTESPEQAEAKPWYEPYILGGVFLQEKGDQLS 210
QY 220 VSVTNEHLIDMDHEAS-FFG 238
DB 211 AEINQPNYLDFAESGQVYFG 230

RESULT 11
ID TNFA_MARMO STANDARD; PRT; 233 AA.
AC O35734;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]

```

SEQUENCE FROM N.A.
TISSUE=Peripheral blood;
MEDLINE=98139533; PubMed=9472070;
Lohrengel B., Lu M., Roggendorf M.,
"Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
and IL-6";
RT and IL-6";
RL Immunogenetics 47:332-335 (1998).
[2]
SEQUENCE FROM N.A.
TISSUE=Peripheral blood;
Zhou H., Hu J., Seeger C.,
Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
TISSUE=Peripheral blood;
MEDLINE=20184746; PubMed=10721723;
Li D.H., Havell E.A., Brown C.L., Cullen J.M.,
"Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
structure, characterization and biological activity";
RL Gene 242:295-305 (2000).
[4]
SEQUENCE FROM N.A.
Hodgson P.D., Michalak T.I.,
"Augmented hepatic interferon gamma expression and T cell influx
characterize acute hepatitis progressing to recovery and residual
lifelong virus persistence in experimental adult woodchuck hepatitis
virus infection";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin 1 secretion and is implicated in the induction of
cachexia. Under certain conditions it can stimulate cell
proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
extracellular soluble form (By similarity).
CC -!- PMW: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
phosphorylated on serine residues. Dephosphorylation of the
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
cancer and infection, and is characterized by general ill health
and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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DR EMBL; Y14137; CAA74569.1; -
DR EMBL; AF082491; AAC32615.1; -
DR EMBL; AF012910; AAF34863.1; -
DR EMBL; AF096268; AAF34867.1; -
DR EMBL; AF333967; AAK52718.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNFPROSISPT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS00419; TNF_2; 1.

KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 233
FT CHAIN 78 233
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT DOMAIN 57 233
FT SITE 77 78
FT MOD_RES 2 2
FT DISULFID 146 177
SQ SEQUENCE 233 AA; 25764 MW; 34D3D1965DAAE0E7 CRC64;
Query Match 9.7%; Score 125; DB 1; Length 233;
Best Local Similarity 23.2%; Pred. No. 0.0028;
Matches 36; Conservative 30; Mismatches 69; Indels 20; Gaps 5;
QY 99 SPSPKNEKALGRKINS-----WSSRSGHSLNLHURNGELVHEKGFYIYSQT 150
DB 80 SSSQNMNDKPAHVAVKNEQELVWLSRRANALLANGMELIDNQLVVPANGLYLVISQV 139
QY 151 YRFQEEIKENTDKQNVQIYKY-TSPDPILLMKSGARNSCKSKDAEYGLYS-----I 204
DB 140 LFKGQ-----GCPSTVLLTHVSRFAVSQDKVLLSAIKSPCKESLEGAEFPKWEPI 194
QY 205 YOGGIFELKENDRIEFSVTNEHLIDMDHEAS-FFG 238
DB 195 YLGGVFELQKGRLSAEVNLPSYLDFAESGQVYFG 229
RESULT 12
TNFA HUMAN STANDARD; PRT; 233 AA.
ID P01375; O43647; Q9P102; Q9UIV3;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=87217060; PubMed=3555974;
RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
Filipov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,
Chumakov A.M., Shingrova L.N., Orzhinnikov Y.A.;
RT "Random arrangement of genes coding for tumor necrosis factor (TNF-
alpha) and lymphotoxin (TNF-beta) in the human genome.";
RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624 (1986).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=85086244; PubMed=6392892;
RA Pennica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R.,
Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;
RT "Human tumour necrosis factor: precursor structure, expression and
homology to lymphotoxin";
RL Nature 312:724-729 (1984).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=85137898; PubMed=3883195;
RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;
RT "Cloning and expression in Escherichia coli of the gene for human
tumour necrosis factor";
RL Nature 313:803-806 (1985).
[4]
SEQUENCE FROM N.A.
RX MEDLINE=86016093; PubMed=2995927;
RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,
Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;


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RA Jones E.Y., Stuart D.I., Walker N.P.;
RT "The structure of tumour necrosis factor -- implications for
RL biological function.";
RN J. Cell Sci. Suppl. 13:11-18(1990).
RP [23]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RA MEDLINE=9008932; PubMed=2551905;
RA Eck M.J., Sprang S.R.;
RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.
RT Implications for receptor binding.";
RL J. Biol. Chem. 264:17595-17605(1989).
RN [24]

Query Match      9.6%; Score 123; DB 1; Length 233;
Best Local Similarity 23.0%; Pred. No. 0.0041;
Matches 43; Conservative 32; Mismatches 70; Indels 42; Gaps 8;

QY      80 GPQR-----VAAHITGRGSRNTLSSPNSK-----NEKALGRKINSWESSRSGH 123
DB      57 GPQREPRDLSTLSPLAQVRSSR---PSDKPVAHVAVNPAEGQL--QWLNRANA 111
QY      124 SFLNLHRLNGELVHKEGFYIYQSYFRPQEEIKENTKNDKQMVYIYKYT-----S 177
DB      112 LLANGVELRDNLQVLPSEGLYIYQVLFKQ-----GCPSTHLLVTHITRIASV 162
QY      178 YPDPIILMKARNSCWSK----DAEGLYSIYGGIFELKENDRIFVSVTNEHLIDMDH 232
DB      163 YQTKVNLISAKSCQRETEGAEAKPWYEPVILGGVQLEKGDRLSAEINRPDYLDFAE 222
QY      233 EAS--FFG 238
DB      223 SGQVYFG 229

RESULT 13
TNFA CEREL
ID TNFA CEREL STANDARD; PRT; 229 AA.
AC PS1743;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin) (Fragment).
GN TNF OR TNFSF2 OR TNFA.
OS Cervus elaphus (TNP deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Lockhart E.A.;
RT "Cloning and sequencing of cervine tumor necrosis factor.";
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
```

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CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DB      EMBL; U14683; AAA50759.1; -.
DB      HSP; P01375; 4TSV.
DB      InterPro; IPR006053; TNF_abc.
DB      InterPro; IPR006052; TNF_family.
DB      InterPro; IPR008983; TNF-like.
DB      InterPro; IPR003636; TNF_subf.
DB      Pfam; PF00229; TNF; 1.
DB      PRINTS; PR01234; TNECROSISFCT.
DB      SMART; SM00207; TNF_1.
DB      PROSITE; PS00251; TNF_1; 1.
DB      PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor.
FT NON_TER 1
FT CHAIN <1 229 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 74 229 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN <1 30 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 31 51 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 52 229 EXTRACELLULAR (POTENTIAL).
FT SITE 72 73 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT DISULFID 141 173 BY SIMILARITY.
SQ SEQUENCE 229 AA; 24987 MW; 16DE5F7AA5A7DB35 CRC64;

Query Match      9.5%; Score 122.5; DB 1; Length 229;
Best Local Similarity 22.8%; Pred. No. 0.0044;
Matches 41; Conservative 35; Mismatches 77; Indels 27; Gaps 7;

QY      80 GPQVAAHITGRGSRNTLSSPNSKNEKALGR-----KINS-----WESSRSGHSFLS 127
DB      52 GPQREQSPSTGLSINSPLVQLRSSQASINKPVAHVAVNINAOQLWLDSKANALMAN 111
QY      128 NULHNGELVHKEGFYIYQSYFRPQEEIKENTKNDKQMVYIYK--YTSYPPILLM 185
DB      112 GVKLEDNQLVWFTDGLYIYQVLFKQ-----SCPSTFLFTHITRIASVYQTKVNL 166
QY      186 KSARNSC-----WSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS--FFG 238
DB      167 SAIKSPCHRETEPWA-EAKPWYEPVYGGVQLEKGDRLSAEINLPDYLDYAESGVYFG 225

RESULT 14
TNFB HUMAN
ID TNFB HUMAN STANDARD; PRT; 205 AA.
AC P01374; Q9UKS8;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE factor ligand superfamily member 1).
GN LTA OR TNFSF1 OR TNFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87217060; PubMed=3555974;
RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
RA Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
RA Filipov S.A., Syrov N.S., Boldyreva E.F., Chuvpilo S.A.,
RA Chumakov A.M., Shangrova L.N., Ovchinnikov Y.A.;
RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-
```

alpha) and lymphotoxin (TNF-beta) in the human genome.";
RT Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86086150; PubMed=3001109;
RA Nedwin G.B., Jarrett-Nedwin J., Smith D.H., Naylor S.L.,
RT Sakaguchi A.Y., Goeddel D.V., Gray P.W.;
EA "Structure and chromosomal localization of the human lymphotoxin
RT gene.";
RN J. Cell. Biochem. 29:171-181(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87057135; PubMed=3536896;
RA Kobayashi Y., Miyamoto D., Asada M., Obinata M., Osawa T.;
RT "Cloning and expression of human lymphotoxin mRNA derived from a
RT human T cell hybridoma.";
RN J. Biochem. 100:727-733(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=85086243; PubMed=6334807;
RA Gray P.W., Aggarwal B.B., Benton C.V., Bringman T.S., Henzel W.J.,
RT Jarrett J.A., Leung D.W., Moffat B., Ng P., Svedersky L.P.,
RA Palladino M.A., Nedwin G.E.;
RT "Cloning and expression of cDNA for human lymphotoxin, a lymphokine
RT with tumour necrosis activity.";
RN Nature 312:721-724(1984).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92339500; PubMed=1353024;
RA Matsuyama N., Okawa N., Tsukil Y., Endo T., Kaji A.;
RT "Nucleotide sequence of a cDNA encoding human tumor necrosis factor
RT beta from B lymphoblastoid cell RPMI 1788.";
RN FEBS Lett. 302:141-144(1992).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93270209; PubMed=8499947;
RA Iris F.J.M., Bougueleret L., Eriur S., Caterina D., Primas G.,
RT Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
RA Cohen D.;
RT "dense Alu clustering and a potential new member of the NF kappa B
RT family within a 90 kilobase HLA class III segment.";
RN Nat. Genet. 3:137-145(1993).
RN [7]
RP SEQUENCE FROM N.A.
RA Neville M.J., Milner C.M., Campbell R.D.;
RT "A new member of the immunoglobulin superfamily and a V-ATPase G
RT subunit are amongst the predicted products of novel genes close to the
RT TNF locus in the human MHC.";
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Shina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
RA Laskey S., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
RT region.";
RN Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A., AND VARIANTS ARG-13; PRO-51 AND ASN-60.
RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND VARIANT ASN-60.
RX MEDLINE=93083656; PubMed=1451807;
RA Voigt C.G., Maurer-Fogy I., Adolph G.R.;
RT "Natural human tumor necrosis factor beta (lymphotoxin). Variable O-
RT glycosylation at Thr7, proteolytic processing, and allelic

variation.";
RT FEBS Lett. 314:85-88(1992).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=92129275; PubMed=1733919;
RA Eck M.J., Ullrich M., Rinderknecht E., de Vos A.M., Sprang S.R.;
RT "The structure of human lymphotoxin (tumor necrosis factor-beta) at
RT 1.9-A resolution.";
RN J. Biol. Chem. 267:2119-2122(1992).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 61-205 OF COMPLEX WITH
RP TNFRI.
RX MEDLINE=93258809; PubMed=8387891;
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Lottschner H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT beta complex: implications for TNF receptor activation.";
RN Cell 73:431-445(1993).
RN [14]
RP VARIANT ASN-60.
RX MEDLINE=91086846; PubMed=1670638;
RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
RA Rietmuller G., Weiss E.H.;
RT "Polymorphic structure of the tumor necrosis factor (TNF) locus: an
RT NcoI polymorphism in the first intron of the human TNF-beta gene
RT correlates with a variant amino acid in position 26 and a reduced
RT level of TNF-beta production.";
RN J. Exp. Med. 173:209-219(1991).
RN [15]
RP VARIANT PRO-125.
RX MEDLINE=91139175; PubMed=1671667;
RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RT "Haplotypic polymorphisms of the TNFB gene.";
RN Immunogenetics 33:50-53(1991).
CC -1- FUNCTION: Cytokine that in its homotrimeric form binds to
CC heterotrimeric form with LTB binds to TNFRSF3/UTER. Lymphotoxin is
CC produced by lymphocytes and cytotoxic for a wide range of tumor
CC cells in vitro and in vivo.
CC -1- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC LTA subunits or (less prevalent) two LTA and one LTB subunits.
CC -1- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC associated (heterotrimers).
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X01393; CAA25649.1; -
CC EMBL; X02911; CAA26670.1; -
CC EMBL; D00102; BAA00064.1; -
CC EMBL; M16441; AAG61199.1; -
CC EMBL; D12614; BAA02139.1; -
CC EMBL; M55913; AAB59455.1; -
CC EMBL; Z15026; CAA78746.1; -
CC EMBL; Y14768; CAA75071.1; -
CC EMBL; AP000505; BAB63397.1; -
CC EMBL; AF129756; AAD18092.1; -
CC EMBL; AY070490; AAL49956.1; -
CC EMBL; AY216498; AAO21135.1; -
CC EMBL; A06316; CAA00536.1; -
CC PIR; A92755; QMHUX.
CC PDB; 1TNR; 31-JUL-94.
CC GlycoSuiteDB; P01374; -
CC Genew; HGNC:6709; LTA.
CC MIM; 153440; -
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.


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QY 72 ISPLVERGQPV-----AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126
Db 70 ISPLAQAGSSSRTPSDKPVAVVA-----NPAEGQL--QWLNRRANALIA 113
QY 127 SNLHNGELAVTHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPD 180
Db 114 NGVELRDNQVLVPSGLYIYSQVLPKQ-----GCPSTHLLTHTISRIAVSYQT 164
QY 181 PILMKSAKNSCWSK-----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
Db 165 KVNLSAIAKSPCQRETPEGAEPWYEPYLGGVFOLEKGDRLSABINEPDPYIDFAESQ 224
QY 236 -FTG 238
Db 225 VYFG 228
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Search completed: June 3, 2004, 09:03:26
Job time : 18 secs


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QY 82 QVAAHITGTRGNT-----LSSPNSKNEKALGRKINSWESSRSHSPISNLHRLNGEL 136
DQ 47 QPRAHLTSSASDNRQRQSDMHQFQDLHSCRHPVHTW-ANKSFGAHLNMTLTNGRL 105
QY 137 VHEKGFYIYSQYFRF-QBEIKENTKNDQMVQYIYKTSYDPDILLMKSAARNSCWSK 195
DQ 106 RVPQDGRYLYSQYFRFSPSDSDQSSVSHQVQCYKTSYLNPIQLLKGVTCKWAP 165
QY 196 DAEGVGLYSYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
DQ 166 DAAYALHSVYQGLFELRAGDEVFVSSTPMVYGEDSSSYFGAF 210

RESULT 2
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas ligand (Fragment).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20010026; PubMed=10540161;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 118:63-70(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR HSP; P50591; 1d4V.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0046020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006913; P:apoptosis; IEA.
DR GO; GO:0006955; P:pimmune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDB3955B014717B6B CRC64;

Query Match 13.6%; Score 175.5; DB 11; Length 169;
Best Local Similarity 27.8%; Pred. No. 5.9e-07;
Matches 54; Conservative 39; Mismatches 58; Indels 43; Gaps 10;

QY 45 QRLVVRKMLTSTSTVQKQONISPLVRERGPGORVAHITGTRGNTLSSPNSK 104
DQ 10 ELRESINQ---RNTPESL---EKQIGHPSSPSDKALRAAHLT---GKPNRSRSP--- 56

QY 105 NEKALGRKINSWESSRSHSPISNLHRLNGELVHEKGFYIYSQYFRFOBEIKENTKN 164
DQ 57 -----LEWEDT-YGSLISGVKYQKGLVINDTGLFYYSKIYFRGQ-----SCN 100

QY 165 DKQMVQYIY-KYTSYDPDILLMK-SARNSC-----WSKDAEYGLYSYQGGIFELKENDR 217
DQ 101 NQPLSHKVYQNSKYPQDLVLMEGKMNYCTTGQWMAW-----SSYLGAVENTFTSNDH 153

QY 218 IFVSVTNEHLIDMD 231
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DB 154 LYVNVSELSLNF 167
Q8MJ19 PRELIMINARY; PRT; 154 AA.
AC Q8MJ19;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas ligand CD178 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaquier J.;
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF530076; AAM95636.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:pimmune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 17410 MW; 971A43779B029449 CRC64;

Query Match 12.2%; Score 157; DB 6; Length 154;
Best Local Similarity 27.4%; Pred. No. 1.9e-05;
Matches 46; Conservative 33; Mismatches 65; Indels 24; Gaps 6;

QY 57 TSEETISTVQKQONISPLVRERGPGORVAHITGTRGNTLSSPNSKNEKALGRKINS 116
DQ 8 TSQKHTASSLEKQIGHPSPPPEKQKVAHLTG-----KPNRSWPL-----EW 52

QY 117 ESSRSGHSLNHLNRLNGELVHEKGFYIYSQYFRFOBEIKENTKNQMVQYIY-KY 175
DQ 53 EDT-YGIVLLSGVKYKGGGLVNETGLFYYSKYVFRGQ-----SCTNPLSHKVMRN 105

QY 176 TSYDPDILLMKSAARNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVT 223
DQ 106 SKYPQDLVMEGKMNS-YCTTGQWMAWSSYLGAVFNLTSADHLYNVNS 152

RESULT 4
Q7T2Q3 PRELIMINARY; PRT; 227 AA.
AC Q7T2Q3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor-3 alpha.
GN TNF-3ALPHA.
```

OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Savan R., Sakai M.,
 RT "Cloning of tumor necrosis factor 3 alpha in carp."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB112424; BAC77690.1; -
 SQ SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;

Query Match 11.8%; Score 151.5; DB 13; Length 227;
 Best Local Similarity 25.3%; Pred. No. 8.7e-05;
 Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7;

QY 75 LVTRERQPVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG 134
 DB 67 LSKENYTSKVAIHLSGA-----YEPDVSKNNIDWKQNDGAFVSGGLKLVDR 113
 QY 135 ELVIHEKGFYIYSQVFRFQBEIKENTKNDKQVQIYKTSYDPD-----PILLMKSA 188
 DB 114 EIIIPNDGIYFISQVSFHI--SKNDMTEDQEVHVSNAVHYSDFGIYKP--LIRAA 169
 QY 189 RNSCW----SKDAEYGLIYSQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
 DB 170 RSACVHASNTEDWYD--TIYLGAFSLRAGDKLCTTKITELLPRVETDNKTFEGVF 225

RESULT 5
 ID 070332 PRELIMINARY; PRT; 216 AA.
 AC 070332;
 DT 01-AUG-1998 (TEMBLrel. 07, Created)
 DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Tumor necrosis factor-alpha (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
 RT analysis of cytokine mRNA expression in experimental visceral
 RL leishmaniasis."
 RL Infect. Immun. 66:2135-2142(1998).
 DR EMBL; AF046215; AAC40100.1; -
 DR HSP; P06804; 2TNF.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006053; TNF-abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PSS0049; TNF_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 216 AA; 23793 MW; BADA3F83F45B533 CRC64;

Query Match 11.2%; Score 144.5; DB 11; Length 216;

Query Match

Best Local Similarity 26.9%; Pred. No. 0.00032;
 Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;

QY 80 GQPVAAH---ITGTRGRSNTLSSPNSKNEKALGRKINS-----WESSRSGHSFLS 127
 DB 49 GQREKFPNPIIGSMGOTLIRSSSSQNSNDKPVGHVVANHQVEQLEWLSHRANALLAN 108
 QY 128 NLHLRNGELVIEHKGFIYSQVFRFQBEIKENTKNDKQVQIYK-----YTSYDP 180
 DB 109 GMSLKDNDQVLPADGLYIVISQVIFRQ-----GQPSYVLLTHTVSRFAVSFED 157
 QY 181 PILLMKSAENSCWSKDAEYGLIYSQGGIFELKENDRIFVSVTNEHLID 229
 DB 158 NVNLLSAIKSPC-PKETPEGEELKWPBYILGVFQLEKGDRLSAEVLNPKYLD 211

RESULT 6
 Q8AW02
 ID Q8AW02 PRELIMINARY; PRT; 231 AA.
 AC Q8AW02;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Putative tumour necrosis factor alpha two.
 DE TNF-ALPHA2PRO.
 GN Cyprinus carpio (Common carp).
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Saeij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,
 RA Wiegertjes G.F.;
 RT "Molecular and functional characterization of carp TNF: Association of
 RT TNF polymorphism with trypanotolerance."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ311801; CAC84642.2; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006053; TNF abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PSS0049; TNF_2; 1.
 DR PROSITE; 231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;
 SQ SEQUENCE 231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;

Query Match 11.0%; Score 141; DB 13; Length 231;
 Best Local Similarity 23.3%; Pred. No. 0.00068;
 Matches 51; Conservative 38; Mismatches 90; Indels 40; Gaps 9;

QY 44 WQRLQVRKMLRTSEETISTVQEKQKN-----ISPLVREGRQPVAAHITGTR 92
 DB 29 WRVCGVLLAVALCAAAAVCFITLNSQNNQEGGNALRLTRDHLKSNVTSKVAIHLTGA- 87
 QY 93 GRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKGFIYSQVTF 152
 DB 88 -----YDPDVCKDNL-----DNKQNDQAFVSGGLELDVREIIPNDGIYFVSVQVSF 135
 QY 153 RFQBEIKENTKNDKQV-----QYIKYTSYDDPILLMKSAENSC-WSKDAEYGLY-S 203
 DB 136 HI--SKNDMTEDQEVHVSNAVHYSDFGIYKP--LPSAIRSACVHASDSDELWYNT 190
 QY 204 IYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
 DB 191 IYLGAFNLARDLRTETTKELLPRVSENGKTFEGVF 229

DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 215 215
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 10.5%; Score 135; DB 6; Length 215;
Best Local Similarity 25.3%; Pred. No. 0.002;
Matches 43; Conservative 31; Mismatches 72; Indels 24; Gaps 5;

QY 80 GPQR--VAAHITGTRGRANTLSSPNSKNEKALGRKINS-----WESSRSGHSFSLNL 129
DB 48 GPQRDEFFDQNLNALLAQTLLRSRTQSDKPVAVHVASIKSEGOLLWESEVANALLANGM 107

QY 130 HLRNGELVTHEKGFYIYSQYVFRQBEIKEN---TKNDKQMVQYIYKYSYPPILLMK 186
DB 108 KLTNDQLVPLDGLYLYISQVLFKQGGCPSTHVLTHNIKRYA-----VSYQKDVNLS 161

QY 187 SARNCSWK----DAEVLGYSIYOGGIFELKENDRIFVSVTNEHLIDMD 231
DB 162 AIKSPQSETPEGABRPWEPYILGVGFQLEKGRDLSAEINLPDYLD 211

RESULT 10
QY Q9ERG6 PRELIMINARY; PRT; 217 AA.
AC Q9ERG6;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peronyscus maniculatus (Deer mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peronyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
RT necrosis factor genes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307013; AAG30264.1; --
DR HSSP; P06804; 2TNF
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 217 217
SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match 10.5%; Score 135; DB 11; Length 217;
Best Local Similarity 24.7%; Pred. No. 0.002;
Matches 43; Conservative 35; Mismatches 72; Indels 24; Gaps 7;

QY 72 ISPLVRGQRVAAHITGTRGRSNTL--SSPNSKNEKALGRKINS-----WESSRSG 122
DB 48 IGPQREKFPNNLP--IIGSMAQTLTLRSSQSSDKPVAVHVAHQVDEQLEWLSRRAN 105

QY 123 HSFLSNLHLRNGELVTHEKGFYIYSQYVFRQBEIKENTKNDKQMVQYIYK-TSYDP 181
DB 106 ALLANGMDLKNQNLVIPADGLYLYISQVLFKQG-----GCSNYVLLTTRVSRFAVSDEK 160

QY 182 ILLKMSARNCSWKDAEYV-----LYSIYOGGIFELKENDRIFVSVTNEHLID 229
DB 161 VNLLSAIKSPC-PKETPEGSELKPWEPYILGVGFQLEKGRDLSAEVNLPKYLD 213

RESULT 11
QY Q7TIU4 PRELIMINARY; PRT; 222 AA.
AC Q7TIU4;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor a.
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Pagrus.
OX NCBI_TaxID=143350;
RN [1]
RP SEQUENCE FROM N.A.
RA Cai Z., Song L., Gao C., Qiu L., Xiang J.;
RT "Cloning and expression of TNFA from Red Seabream (Pagrus major).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY314010; AAP76392.1; --
SQ SEQUENCE 222 AA; 24382 MW; 8D8496F855A552 CRC64;

Query Match 10.1%; Score 130.5; DB 13; Length 222;
Best Local Similarity 24.4%; Pred. No. 0.0049;
Matches 48; Conservative 33; Mismatches 91; Indels 25; Gaps 8;

QY 56 RTSEETISTVQEKQONISPLVRGQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS 115
DB 37 QTALTKTIDTAETKIDPHSTLRLRISAKAAHLEGSYDEDE-----GSKDQV-----G 84

QY 116 WESSRSGHSFL-SNLHLRNGELVTHEKGFYIYSQYVFRQ-----BEIKENTKNDKQMVQ 170
DB 85 WKSGQ-QQAFAGQGFRLVDNKVIPQTGLYFYVSQAFVSCSDGEEGAGHHTPLSHR 143

QY 171 YIYKYSYPPILLMKARNSC--WSKDARY-----GLY-SIYOGGIFELKENDRIFVSVT 223
DB 144 ISRSSESMGSDVSLMSAVRSACNTAQDSDSYSGRGWYNTIYLGAVFQLNRGDLWTETN 203

QY 224 NEHLIDMDHSAFFGAF 240
DB 204 QLSELETEEGKTFPGVF 220

RESULT 12
QY Q8JG37 PRELIMINARY; PRT; 230 AA.
AC Q8JG37;
DT 01-OCT-2003 (TREMELrel. 22, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor.
GN TNF.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou J., Chinchar G., Long S., Miller N., Seconbes C.J.;
RT "Cloning and expression of a tumor necrosis factor homologue in
RT catfish, Ictalurus punctatus."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417565; CAD10389.2; --

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DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
DR SEQUENCE 230 AA; 25598 MW; 3A40D391F75DB019 CRC64;

Query Match 9.8%; Score 126.5; DB 13; Length 225;
Best Local Similarity 22.0%; Pred. No. 0.011;
Matches 42; Conservative 40; Mismatches 78; Indels 31; Gaps 8;

QY 124 SFSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVYIKYTSYPPIL 183
DB 104 SFSGKLEDEIKLRDLGVYSQASYRLCK-AGDETEGEVHMHSKVSWSYS 162
QY 184 ----LMKSARNSCWSDAEYGLY----SIYQGIPELKENDRIFVSVTNEHLIDMDEA-- 234
DB 163 SWKPLLSATRSACKTTEBYQYWGAVYLGAFLNKGADRL-RTVMDEKLLPKVESAGG 221
QY 235 -SFGCAF 240
DB 222 KTFGTF 228

RESULT 13
Q9IB42 PRELIMINARY; PRT; 225 AA.
ID Q9IB42
AC Q9IB42
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 25, Last annotation update)
DE Tumor necrosis factor.
OS Paralichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20491932; PubMed=11035080;
RA Hirono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular Cloning, Characterization, and Expression of TNF cDNA and
RL Gene from Japanese Flounder Paralichthys olivaceus.";
J. Immunol. 165:4423-4427(2000).
DR EMBL; AB040448; BAA94969.1; -.
DR HSSP; P01375; 4TSV.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
DR SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

Query Match 9.8%; Score 126.5; DB 13; Length 225;
Best Local Similarity 22.0%; Pred. No. 0.011;
Matches 42; Conservative 40; Mismatches 78; Indels 31; Gaps 8;

QY 67 EKQONT-SPLVREGRGPORVAHITGTRGNTLSSPNS----KNEKALGRKINSWESSRSGH 123

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DB 47 EKTEPHNTLRQISSRAKAAIHLEG-RDEEDSETSENKLVWKNDEGLA-----FTQGGF 98
QY 124 SFSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVYIKYTSYPPIL 176
DB 99 ELVDN-----HIIPRGLYFVYSQASFRVSCSSDDADDGKAAEKHLTGISHERVWLFT 152
QY 177 -SYPPILLMKASARNSCWSDAEYGLYSIYQGIPELKENDRIFVSVTNEHLID 229
DB 153 ESLGTQVSLMSAVRSACKSQEDAYRDCQGWYNAIYLGAFLNKGADRL-RTVMDEKLLPKVESAGG 212
QY 230 MDHEASFFCAF 240
DB 213 TESGKTFRGVF 223

RESULT 14
Q99ND1 PRELIMINARY; PRT; 215 AA.
ID Q99ND1
AC Q99ND1
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Tumor necrosis factor (Fragment).
OS Tamiasciurus hudsonicus (American red squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamiasciurus.
OX NCBI_TaxID=10009;
RN [1]
RP SEQUENCE FROM N.A.
RX van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RL their sister group.";
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286824; CAC28540.1; -.
DR HSSP; P68804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
DR NON_TER 1 215
FT NON_TER 215
SQ SEQUENCE 215 AA; 23739 MW; 36441309C45E9898 CRC64;

Query Match 9.7%; Score 125; DB 11; Length 215;
Best Local Similarity 24.3%; Pred. No. 0.013;
Matches 35; Conservative 29; Mismatches 62; Indels 18; Gaps 4;

QY 99 SPSNSKNEKALGRKINS-----WESSRSGHFLNHLRNGELVIHEKGFYIYSQTY 151
DB 71 SSSQNMNDKFAVHVANQTEBQQLNLSRRANALLANGMELIDQLVVPADGLYIYSQVL 130
QY 152 FRFOEIKENTKNDKQVYIKY-TSYPPILLMKASARNSCWSDAEYGLY-----IY 205
DB 131 FKQ-----CCSSVLLTHVTSRFAVSQYQDKVLLSAIKSPCKESLEGAEKPKWPEIY 185
QY 206 QGIFELKENDRIFVSVTNEHLID 229
DB 186 LGGVFELQKGRDLSAEVNLPSYLD 209

RESULT 15

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Q9BEC4
ID Q9BEC4 PRELIMINARY; PRT; 216 AA.
AC Q9BEC4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Talpa europaea (European mole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
OX NCBI_TaxID=9375;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RL their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286831; CAC28539.1; -
DR HSSP; P01375; 1A8M.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005154; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_family.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNFCROSISPECT.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23542 MW; FPFEP8DBBD27836 CRC64;

Query Match 9.6%; Score 124; DB 6; Length 216;
Best Local Similarity 21.8%; Pred. No. 0.016; Indels 24; Gaps 5;
Matches 38; Conservative 37; Mismatches 75;
QY 66 OEKQNIQPLVREGPQ-RVAAHITGTRSGNTLSSPNSKNEKALGRKINSWESSRSGHS 124
DB 51 EEQHTLPLNTLAQLRSSRTGDKPVAHVANPQAEGL-----QWLSQVANAL 103
QY 125 FLNHLNKGELVTHEKGYIYSQTYFRQEEIKENTKNDKQVQIYKY-----TSYPD 180
DB 104 LANGVELTNQNLVPSDGLIYISQVLFKQ-----GCPENLVLLTHKIQRTAVSYED 156
QY 181 PILLMKARNCSWK-----DAEYGLYSIYOGGIFELKENDRIFVSVTNEHLID 229
DB 157 AVDLLSAIKSPQRETPEGAERPWYEPYILGGVPLEKGRLSANINLPKYLD 210

Search completed: June 3, 2004, 09:04:24
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:56:26 ; Search time 59 Seconds
(without alignments)
1163.713 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYKSGIACFL.....NEHLIDMDHEASFFGAFVVG 243

Scoring table: BLCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1166853

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	953.5	74.1	220	3	AAV88630 Cell fact
2	907	70.5	173	5	ABG72258 Partial h
3	887	68.9	168	4	ABG76826 Human TRA
4	887	68.9	168	5	AAU99896 Human TNF
5	882	68.5	168	5	ABG72259 Partial h
6	878	68.2	166	3	AAU808274 Amino aci
7	866	67.3	167	6	ABR84402 TRAIL ami
8	850	66.0	161	4	AAV71985 C-termina
9	850	66.0	161	6	ABR39855 TNF famil
10	850	66.0	161	7	ADC03335 Tumour ne
11	827	64.3	212	5	AAU99301 Human TRA
12	746.5	58.0	188	5	AAU79599 Human TRA
13	727	56.5	139	2	AAV01518 Polypepti
14	633	49.2	172	3	AAU808275 Amino aci
15	425	33.0	121	3	AAU803752 Human sec
16	370	28.7	113	5	AAU79600 Human TRA
17	291	22.6	98	5	AAU79595 Human TRA
18	291	22.6	101	2	AAU19790 Human apo
19	291	22.6	101	2	AAU56761 Human TRA
20	291	22.6	101	4	AAE11032 Human TRA
21	291	22.6	101	6	AAU08559 Human TNF
22	278	21.6	56	5	AAE23263 Protein #
23	277	21.5	88	5	AAU79594 Human TRA
24	236	18.3	178	6	ADA50080 Human wil
25	233.5	18.1	199	5	ABG94285 Mouse RAN

26	233.5	18.1	199	5	ABG80597	Mouse rec
27	232.5	18.1	152	4	ABG67248	Human RAN
28	232.5	18.1	160	3	AAU08273	Amino aci
29	232.5	18.1	185	5	ABG94338	Human C-R
30	232.5	18.1	185	5	ABG80650	Human RAN
31	232.5	18.1	186	5	ABG71829	Human RAN
32	232.5	18.1	200	5	ABG71827	Human RAN
33	232.5	18.1	216	7	ADB16998	Human RAN
34	230.5	17.9	170	4	AAU08386	Mouse PLA
35	230.5	17.9	216	7	ADB16999	Murine RA
36	228.5	17.8	155	6	ABR39854	RANK liga
37	228.5	17.8	155	7	ADC03334	Murine re
38	228.5	17.8	160	3	AAU08272	Amino aci
39	228.5	17.8	173	3	AAV84422	A murine
40	228.5	17.8	173	3	AAV84421	Amino aci
41	228.5	17.8	187	3	AAV84420	Amino aci
42	219	17.0	139	3	AAV91023	Mouse ORM
43	210	16.3	182	3	AAV84424	An osteop
44	208	16.2	188	3	AAV84423	An osteop
45	202.5	15.7	173	3	AAV84426	An osteop

ALIGNMENTS

RESULT 1

AAV88630
ID AAV88630 standard; protein; 220 AA.

XX AC AAV88630;

XX DT 22-AUG-2000 (first entry)

XX DE Cell factor derivative TRAILD amino acid sequence.

XX KW Cell factor derivative; TRAILD; anticancer; cancer; liver; breast;

XX XM kidney; leukaemia.

XX OS Unidentified.

XX PN CN1243748-A.

XX PD 09-FEB-2000.

XX PF 28-JUL-1999; 99CN-00111039.

XX PR 28-JUL-1999; 99CN-00111039.

XX (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.

XX Zheng D, Liu Y, Ma Z;

XX WPI; 2000-351201/31.

XX New cell factor derivative causing cells to die, for anticancer therapy.
XX Disclosure; Page 2; 10pp; Chinese.
XX The present invention relates to a cell factor derivative (TRAILD) used as an anticancer derivative. The TRAIL protein can be expressed in a soluble form in bacterial cytoplasm. The present sequence represents a TRAILD amino acid sequence. Recombinant TRAILD fusion proteins can be used in anti-cancer medications to treat cancer of the liver, breast, or kidney. It can also be used to treat leukaemia

SQ Sequence 220 AA;

Query Match 74.1%; Score 953.5; DB 3; Length 220;

Best Local Similarity 97.9%; Pred. No. 7.4e-85;

Matches 185; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 56 RTSETISTYOEKQONISPLVRGPGORVAHITGTRGRNTLSSPNKNEKALGRKINS 115

Db 32 KTSEETISTVQKQNISPLVRERGQPVAAHITGRSNTLSSPNSKNEKALGRKINS 91
QY 116 WESSRSGHSFSLNHLRNGELVIH-EKGFYIYISQTYFRQOEIKENTKNDKQWQVIYK 174
Db 92 WESSRSGHSFSLNHLRNGELVIH-EKGFYIYISQTYFRQOEIKENTKNDKQWQVIYK 151
QY 175 YTSYPPDPILLMKARSNCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
Db 152 YTSYPPDPILLMKARSNCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 211
QY 235 SFFGGAFLVG 243
Db 212 SFFGGAFLVG 220
RESULT 2
ABG72258
ID ABG72258 standard; protein; 173 AA.
XX AC ABG72258;
XX DT 04-MAR-2003 (first entry)
XX DE Partial human Trail protein, Trail109.
XX KW Human; tumour related apoptosis inducing ligand; Trail109;
XX KW Trail prokaryotic expression system; tumour cell death.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 109
XX FT /note= "Encoded by CTT"
XX PN CN1354183-A.
XX PD 19-JUN-2002.
XX PF 30-NOV-2001; 2001CN-00132371.
XX PR 30-NOV-2001; 2001CN-00132371.
XX PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
XX PI Hu Y, Yao Y;
XX DR WPI: 2002-751439/82.
XX DR N-PSDB; ABX14392.
XX PT Tumor death induction ligand gene, gene expression protein and its
XX PS preparation method.
XX PS Claim 7; Page 10 (disclosure); 17pp; Chinese.
XX CC The present invention relates to the isolation of cDNA encoding human
XX CC tumour related apoptosis inducing ligand (Trail), and the Trail protein.
XX CC The Trail full length cDNA is cloned, and is utilised to create a Trail
XX CC prokaryotic expression system. The full length Trail cDNA is used to
XX CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
XX CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
XX CC expression systems. The prokaryotic expression systems created greatly
XX CC increase the expression and quantity of the Trail, Trail109, and Trail114
XX CC proteins, and may be useful in a new preparation for killing tumour
XX CC cells. The present sequence represents the partial human Trail protein,
XX CC Trail109
XX SQ Sequence 173 AA;
Query Match 70.5%; Score 907; DB 5; Length 173;
Best Local Similarity 99.4%; Pred. No. 1.9e-80;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 71 NISPLVRERGQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHL 130

Db 1 NISPLVRERGQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHL 60
QY 131 LINGELVTHEKGPYIYISQTYFRQOEIKENTKNDKQWQVIYKTSYPPDPILLMKARSN 190
Db 61 LRNGELVTHEKGPYIYISQTYFRQOEIKENTKNDKQWQVIYKTSYPPDPILLMKARSN 120
QY 191 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGGAFLVG 243
Db 121 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGGAFLVG 173
RESULT 3
ABB76826
ID ABB76826 standard; protein; 168 AA.
XX AC ABB76826;
XX DT 16-JUL-2002 (first entry)
XX DE Human TRAIL.
XX KW Human; TRAIL; tumour necrosis factor; TNF;
XX KW tumour necrosis factor related apoptosis inducing ligand; TRAIL; cancer;
XX KW viral infection; cytostatic.
XX OS Homo sapiens.
XX PN KR2001019100-A.
XX PD 15-MAR-2001.
XX PF 25-AUG-1999; 99KR-00035354.
XX PR 25-AUG-1999; 99KR-00035354.
XX PA (DONG-) DONG WHA PHARM IND CO LTD.
XX PI Cha SS, Kim JU, Lee GJ, Lim GM, Oh BH, Yoon JI, Yoon SJ;
XX DR WPI: 2001-533833/59.
XX DR N-PSDB; ABLS3386.
XX PT Producing and crystallizing tumor necrosis factor related apoptosis
XX PS inducing ligand protein, and its three-dimensional structure.
XX PS Claim 1; Page 14; 20pp; Korean.
XX CC The present invention relates to a method for producing Tumour Necrosis
XX CC Factor (TNF) Related Apoptosis Inducing Ligand (TRAIL) protein, and for
XX CC crystallising the TRAIL protein and its three-dimensional structure,
XX CC where the TRAIL protein has improved activity, which specifically kills
XX CC cancer cells and cells infected by virus. The present sequence is human
XX CC TRAIL, which was used in the invention
XX SQ Sequence 168 AA;
Query Match 68.9%; Score 887; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.6e-78;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 VREGRQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 135
Db 1 VREGRQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60
QY 136 LVTHEKGFYIYISQTYFRQOEIKENTKNDKQWQVIYKTSYPPDPILLMKARSNCWSK 195
Db 61 LVTHEKGFYIYISQTYFRQOEIKENTKNDKQWQVIYKTSYPPDPILLMKARSNCWSK 120
QY 196 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGGAFLVG 243
Db 121 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGGAFLVG 168

Db 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 5

ABG72259

ID ABG72259 standard; protein; 168 AA.

XX AC ABG72259;

XX DT 04-MAR-2003 (first entry)

XX DE Partial human Trail protein, Trail114.

XX KW Human; tumour related apoptosis inducing ligand; Trail114;

XX KW Trail prokaryotic expression system; tumour cell death.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Misc-difference 104 /note= "Encoded by CTT"

XX PN CN1354183-A.

XX PD 19-JUN-2002.

XX PF 30-NOV-2001; 2001CN-00132371.

XX PR 30-NOV-2001; 2001CN-00132371.

XX PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.

XX PI Hu Y, Yao Y;

XX DR WPI; 2002-751439/82.

XX DR N-PSDB; ABX14393.

XX PT Tumor death induction ligand gene, gene expression protein and its preparation method.

XX PS Claim 7; Page 10 (disclosure); 17pp; Chinese.

CC The present invention relates to the isolation of cDNA encoding human tumour related apoptosis inducing ligand (Trail), and the Trail protein. The Trail full length cDNA is cloned, and is utilised to create a Trail prokaryotic expression system. The full length Trail cDNA is used to respectively clone cDNA of soluble ectocytic segment Trail109 and Trail 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic expression systems. The prokaryotic expression systems created greatly increase the expression and quantity of the Trail, Trail109, and Trail114 proteins, and may be useful in a new preparation for killing tumour cells. The present sequence represents the partial human Trail protein, Trail114

XX SQ Sequence 168 AA;

Query Match 68.5%; Score 882; DB 5; Length 168;

Best Local Similarity 99.4%; Pred. No. 5.1e-78;

Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 76 VREGRQVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGE 135

DB 1 VREGRQVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGE 60

QY 136 LVIEHKGFFYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAENSCWSK 195

DB 61 LVIEHKGFFYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAENSCWSK 120

QY 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

DB 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 4

AAU99896

ID AAU99896 standard; protein; 168 AA.

XX AC AAU99896;

XX DT 21-OCT-2002 (first entry)

XX DE Human TNF related apoptosis including ligand (TRAIL) protein.

XX KW TRAIL; TNF receptor apoptosis including ligand; human; SDR5;

XX KW tumour necrosis factor; crystal structure; TRAIL-SDR5 complex; apoptosis.

XX OS Homo sapiens.

XX PN WO200253727-A1.

XX PD 11-JUL-2002.

XX PF 10-JAN-2001; 2001WO-KR000034.

XX PR 29-DEC-2000; 2000KR-00085947.

XX PA (DONG-) DONG WHA PHARM IND CO LTD.

XX PA (UYPO-) UNIV POHANG SCI & TECHNOLOGY.

XX PI Chung YH, Ryu JM, Hwang YH, Yoon JI, Lim KM, Oh B, Cha S;

XX DR WPI; 2002-583613/62.

XX PT Novel expression vector containing an SDR5 encoding gene transformed into Escherichia coli to produce SDR5 protein for crystallizing a tumor necrosis factor-related apoptosis-inducing ligand-SDR5 complex.

XX PS Claim 5; Page 70; 74pp; English.

CC This invention relates to an expression vector containing the tumour necrosis factor related apoptosis inducing ligand (TRAIL) protein receptor SDR5. The invention also comprises a method for producing the SDR5 protein from an E. coli transformed with the vector. The method of the invention is useful for crystallizing the TRAIL-SDR5 complex. A TRAIL-SDR5 crystal complex is useful for developing recombinant proteins i.e. proteins with improved stability or cytotoxic activity of a TRAIL protein which involves changing the amino acid of the AA loop to increase the various interactions between amino acids or from the binding site of metal ions or the disulfide bonding, or changing the corresponding amino acids of the homotrimer interface or homodimer interface to increase the various interactions between amino acids or from the binding site of metal ion or disulfide bond, or to fill the cavity. A 3 dimensional structure of the TRAIL-SDR5 complex is useful for the molecular strategy conferring specificity for the recognition between TNF family members and TNF receptor family members and for the development of TRAIL protein, which has a better stable, cytotoxic activity or an improved receptor binding affinity. The present sequence represents the human tumour necrosis factor receptor apoptosis including ligand (TRAIL) protein sequence used in the invention

XX SQ Sequence 168 AA;

Query Match 68.9%; Score 887; DB 5; Length 168;

Best Local Similarity 100.0%; Pred. No. 1.6e-78;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VREGRQVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGE 135

DB 1 VREGRQVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGE 60

QY 136 LVIEHKGFFYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAENSCWSK 195

DB 61 LVIEHKGFFYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAENSCWSK 120

QY 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

```
RESULT 6
AAB08274
ID AAB08274 standard; protein; 166 AA.
XX AC AAB08274;
XX DT 04-DEC-2000 (first entry)
XX DE Amino acid sequence of a human TNF ligand TRAIL.
XX KW AGP-3; tumor necrosis factor ligand; TNF ligand; Crohn's disease;
XX KW type II transmembrane protein; B cell stimulatory factor;
XX KW inflammatory disorder; immune disorder; rheumatoid arthritis;
XX KW lupus and graft versus host disease.
XX OS Homo sapiens.
XX PN WO200047740-A2.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US003653.
XX PR 12-FEB-1999; 9SUS-0119906P.
XX PR 18-NOV-1999; 9SUS-0166271P.
XX PA (AMGE-) AMGEN INC.
XX PI Boyle WJ, Hsu H;
XX PS WPI; 2000-558217/51.
XX CC AAB08265-83 represent tumor necrosis factor (TNF) ligands. The
XX CC specification describes an AGP-3 polypeptide, which is TNF ligand family
XX CC member. AGP-3 is a type II transmembrane protein, and is a potent B cell
XX CC stimulatory factor. Expression of AGP-3 correlates to increases in the
XX CC number of B cells and immunoglobulins produced. AGP-3 proteins,
XX CC antibodies, and nucleic acids may be used to treat inflammatory and
XX CC immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and
XX CC graft versus host disease. The nucleic acids may be used to regulate the
XX CC expression of an AGP-3 related protein. The AGP-3 proteins, antibodies
XX CC and nucleic acids are also useful for the detection of AGP-3 agonists,
XX CC antagonists and characterizing interactions with AGP-3 related proteins
XX CC
XX SQ Sequence 166 AA;
Query Match 58.2%; Score 878; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e-77; Mismatches 0; Indels 0; Gaps 0;
Matches 166; Conservative 0;
QY 78 ERGPQVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV 137
DB 1 ERGPQVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV 60
QY 138 IHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSKDA 197
DB 61 IHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSKDA 120
QY 198 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
DB 121 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 166
RESULT 7
ABR84402
ID ABR84402 standard; protein; 167 AA.
XX AC ABR84402;
XX DT 09-OCT-2003 (first entry)
XX DE TRAIL amino acid sequence.
XX KW TRAIL; TNF-related apoptosis-inducing ligand; tumour; necrosin.
XX OS Unidentified.
XX PN CN1380339-A.
XX PD 20-NOV-2002.
XX PF 10-APR-2001; 2001CN-00105946.
XX PR 10-APR-2001; 2001CN-00105946.
XX PA (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.
XX PI Li B, Gao X, Liu Z;
XX PS WPI; 2003-230973/23.
XX DR N-PSDB; ACC83357.
XX CC Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for
XX CC inducing the death of tumor cells, is related to mutational human tumor
XX CC necrosin.
XX PS Claim 4; Fig 2; 14pp; Chinese.
XX CC The invention relates to a TNF-related apoptosis-inducing ligand encoding
XX CC (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is
XX CC related to mutational human tumor necrosin. The polypeptide of the
XX CC invention is useful for inducing the death of tumor cells. The current
XX CC sequence represents the TRAIL amino acid sequence
XX SQ Sequence 167 AA;
Query Match 67.3%; Score 866; DB 6; Length 167;
Best Local Similarity 98.2%; Pred. No. 1.9e-76; Mismatches 1; Indels 2; Gaps 1;
Matches 166; Conservative 1;
QY 75 LVREGPQVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNG 134
DB 1 LVREERG--RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNG 58
QY 135 ELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWS 194
DB 59 ELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWS 118
QY 195 KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
DB 119 KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 167
RESULT 8
AAY71985
ID AAY71985 standard; protein; 161 AA.
XX AC AAY71985;
XX DT 28-MAR-2001 (first entry)
XX DE C-terminal region of human TRAIL protein.
XX KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
XX KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
XX KW haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;
```

KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 2..8
 FT /label= Beta_strand
 FT Region 32..34
 FT /label= Beta_strand
 FT Region 42..44
 FT /label= Beta_strand
 FT Region 47..50
 FT /label= Beta_strand
 FT Region 53..56
 FT /label= Beta_strand
 FT Region 61..72
 FT /label= Beta_strand
 FT Region 86..91
 FT /label= Beta_strand
 FT Region 99..109
 FT /label= Beta_strand
 FT Region 118..128
 FT /label= Beta_strand
 FT Region 133..143
 FT /label= Beta_strand
 FT Region 153..160
 FT /label= Beta_strand
 XX
 PN WO20068378-A1.
 XX
 PD 16-NOV-2000.
 XX
 XX 05-MAY-2000; 2000WO-US012266.
 XX
 XX 06-MAY-1999; 99US-0132892P.
 PR 01-MAY-2000; 2000US-0201012P.
 XX
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 FA
 XX
 XX Shu HS;
 PI
 XX WPI; 2001-016094/02.
 DR
 XX
 XX Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 FT autoimmune disorders.
 PT
 XX
 PS Example 1; Fig 1b; 112pp; English.
 XX
 XX The present invention relates to Tumour necrosis factor (TNF) and ApoL-
 CC related leucocyte expressed ligand 1 (TALL-1) nucleic acid molecules,
 CC proteins (including homologues), and their antibodies. The invention in
 CC particular relates to methods for regulating the interaction between TALL
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
 CC TALL-1 protein is useful for identifying compounds that regulate B
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte
 CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.
 CC The present sequence is a C-terminal region of human TRAIL protein, which
 CC has 20-25% sequence identity with the C-terminal region of human TALL-1
 CC protein extracellular domain. TRAIL protein is a TNF family member
 XX
 XX Sequence 161 AA;
 XX
 XX Query Match 66.0%; Score 850; DB 4; Length 161;
 XX Best Local Similarity 100.0%; Pred. No. 6.5e-75;
 XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 142
 DB 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 60
 QY 143 FYIYSOTYPRFQEEIKENTKDKOMQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 202
 DB 61 FYIYSOTYPRFQEEIKENTKDKOMQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 120
 QY 203 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 243
 DB 121 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 161
 RESULT 9
 ABR39855
 ID ABR39855 standard; protein; 161 AA.
 XX
 AC ABR39855;
 XX
 XX 11-AUG-2003 (first entry)
 DT
 XX TNF family member, TRAIL (1d4v) protein fragment.
 DE
 XX RANK, receptor activator of necrosis factor kB; RANK ligand; RANKL;
 KW tumour necrosis factor; TNF; TRAIL; cytokine.
 KW
 XX Unidentified.
 OS
 XX WO2003014077-A2.
 FN
 XX 20-FEB-2003.
 PD
 XX 09-AUG-2002; 2002WO-US025287.
 PF
 XX 09-AUG-2001; 2001US-0311163P.
 PR
 XX 22-MAR-2002; 2002US-00105057.
 PR
 XX (BARN-) BARNES-JEWISH HOSPITAL.
 PA
 XX
 XX Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
 PI
 XX WPI; 2003-256526/25.
 XX
 XX Composition for identifying a compound with Receptor Activator of
 PT Necrosis Factor KB, RANK modulating activity and for identifying RANK or
 FT osteoprotegerin modulating compound, has a protein complex in crystalline
 PT form.
 PT
 XX
 XX Disclosure; Fig 3; 66pp; English.
 PS
 XX The invention relates to a composition (I) comprising a protein complex
 CC in crystalline form, where the complex comprises an amino acid sequence
 CC of a Receptor Activator of Necrosis Factor KB (RANK) Ligand (RANKL)
 CC ectodomain. (I) is useful for identifying a compound with RANK modulating
 CC activity, and for identifying a RANK or OPG modulating compound. (I) is
 CC useful to intelligently design mutants that have altered biological
 CC properties and for identifying and/or designing compounds that bind RANK
 CC as an approach towards developing new therapeutic agents. (I) is also
 CC useful to computationally screen small molecule databases for chemical
 CC entities or compounds that can bind in whole, or in part, to RANK or
 CC RANKL. The present sequence represents a tumour necrosis factor (TNF)
 CC family member, TRAIL (1d4v), used in a structural-based alignment study
 CC of murine RANKL protein
 XX
 XX Sequence 161 AA;
 XX
 XX Query Match 66.0%; Score 850; DB 6; Length 161;
 XX Best Local Similarity 100.0%; Pred. No. 6.5e-75;
 XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 142

Db 1 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 60
QY 143 FYIYISQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 202
Db 61 FYIYISQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
RESULT 10
ADCO3335
ID ADCO3335 standard; protein; 161 AA.
XX
AC ADCO3335;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour necrosis factor family cytokine, TRAIL.
XX
KW RANKL ectodomain crystal complex; RANK; osteoprotegerin; OPg;
KW bone-forming compound; tumour necrosis factor; TNF family; cytokine;
KW TRAIL.
XX
OS Mus sp.
XX
PN US2003050223-A1.
XX
PD 13-MAR-2003.
XX
PE 09-AUG-2002; 2002US-00215446.
XX
PR 09-AUG-2001; 2001US-0311163P.
XX
PA (LAMJ//) LAM J.
PA (ROSS//) ROSS F P.
PA (TEIT//) TEITELBAUM S L.
PA (NELS//) NELSON C A.
PA (FREM//) FREMONT D H.
XX
FI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
XX WPI; 2003-605763/57.
XX
XX Composition comprising crystalline receptor activator of NF-kappaB (RANK)
XX ligand ectodomain complex whose three-dimensional structural
XX representation is useful for identifying RANK or osteoprotegerin
XX modulating compound.
XX
XX Disclosure; Fig 3; 40pp; English.
XX
XX The invention relates to a composition comprising a protein complex in
XX crystalline form, where the complex comprises an amino acid sequence of a
XX receptor activator of nuclear factor kappaB (NF-kappaB) (RANK) ligand
XX (RANKL) ectodomain. The three-dimensional structural representation of a
XX RANKL ectodomain crystal complex, is useful for identifying a RANK or
XX osteoprotegerin (OPG) modulating compound, and for identifying a compound
XX with RANK modulating activity. The crystals permit the determination of
XX the three-dimensional X-ray diffraction structure of the crystal-line
XX polypeptide to high resolution. The atomic structure coordinates and
XX structural information which comprises atomic structure coordinates are
XX useful for identifying bone-forming compounds by methods which utilise
XX the coordinates for solving the three-dimensional X-ray diffraction
XX and/or solution structures of other proteins, including mutant forms, to
XX high resolution. The structural information may also be used in a variety
XX of molecular modeling and computer-based screening applications to, for
XX example design mutants of the crystallized RANKL, its receptors, or a
XX portion or fragment of RANKL or its receptors. The coordinates of RANKL
XX crystal, or subsets of such structural coordinates of the RANKL crystal,
XX are useful for designing or identifying candidate compounds capable of
XX modulating RANK biological activity, and for identifying compounds which

CC mimic the capability of RANKL to bind RANK molecules, thereby activating
CC the receptor. The present sequence represents the amino acid sequence of
CC the tumour necrosis factor family cytokine, TRAIL.
XX
SQ Sequence 161 AA;
Query Match 66.0%; Score 850; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 142
Db 1 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 60
QY 143 FYIYISQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 202
Db 61 FYIYISQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
RESULT 11
AAU99301
ID AAU99301 standard; protein; 212 AA.
XX
AC AAU99301;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human TRAIL splice variant 8, rpl-6-6, protein.
XX
KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26; rpl-6-6.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..16 /note= "Cytoplasmic domain"
FT Domain 17..38 /note= "Transmembrane domain"
FT Domain 39..212 /note= "Extracellular domain"
FT Misc-difference 209 /note= "Encoded by in-frame stop codon"
XX
XX US2002061525-A1.
XX
XX 23-MAY-2002.
XX
XX 16-MAY-2001; 2001US-00855544.
XX
XX 16-MAY-2000; 2000IL-00136156.
XX
XX (YELI//) YELIN R.
XX (KHOS//) KHOSRAVI R.
XX (SAVI//) SAVITZKY K.
XX
XX Yelin R, Khosravi R, Savitzky K;
XX WPI; 2002-479259/51.
XX
XX New splice variants of tumor necrosis factor-related apoptosis inducing
XX ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
XX diseases or disorders associated with low expression of the variants.
XX

Db 39 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESNPGQVWOLQOLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 120
Db 99 TISTVQ----- 104
QY 121 SGHSPLSLNHLNGLVTHKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSPD 180
Db 105 -----ENTKNDKQWQVIYKYTSPD 125
QY 181 PILLKMSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 126 PILLKMSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185
QY 241 LVG 243
Db 186 LVG 188
RESULT 13
AAV01518
ID AAV01518 standard; peptide; 139 AA.
XX AC AAV01518;
XX DT 27-MAY-1999 (first entry)
XX DE Polypeptide of the invention.
XX KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
KW surface receptor; TRAIL protein.
XX OS Homo sapiens.
XX PN FR2766713-A1.
XX PD 05-FEB-1999.
XX PF 04-AUG-1997; 97FR-00010176.
XX PR 04-AUG-1997; 97FR-00010176.
XX PA (INMR) BIO MERIEUX.
XX PI Rieger F, Belliveau JF, Perron H;
XX WPI; 1999-156177/14.
XX PT Use of polypeptide derived from TRAIL protein for diagnosis of
PT degenerative disease - autoimmunity and inflammation, also useful in
PT prevention or treatment, and similar use of corresponding ligand and
PT nucleic acid.
XX PS Claim 5; Page 14; 21pp; French.
XX CC The specification describes the use a polypeptide corresponding to at
CC least the primary sequence of part AAV01516-17 to produce a diagnostic,
CC prophylactic or therapeutic composition useful in cases of degenerative,
CC autoimmune and inflammatory diseases. The polypeptides can be used in
CC treatment of neurodegenerative diseases, lupus erythematosus, rheumatoid
CC arthritis, and SEP. The polypeptides are apoptotic in central nervous
CC system cells, antigenic and specifically recognise the surface receptor
CC of the TRAIL protein. The polypeptide is a marker of disease and a
CC therapeutic target, e.g. its apoptotic activity can be blocked with an
CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex. The present sequence
XX represents a polypeptide of the invention
SQ Sequence 139 AA;

Query Match 56.5%; Score 727; DB 2; Length 139;

Best Local Similarity 100.0%; Pred. No. 5.9e-63;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 TSEETISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 116
Db 1 TSEETISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 60
QY 117 ESSRSGHSPLSLNHLNGLVTHKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKYT 176
Db 61 ESSRSGHSPLSLNHLNGLVTHKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKYT 120
QY 177 SYPDPIILLKMSARNSCWSK 195
Db 121 SYPDPIILLKMSARNSCWSK 139
RESULT 14
AAB08275
ID AAB08275 standard; protein; 172 AA.
XX AC AAB08275;
XX DT 04-DEC-2000 (first entry)
XX DE Amino acid sequence of a mouse TNF ligand TRAIL.
XX KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.
XX OS Mus sp.
XX PN WO2000047740-A2.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US003653.
XX PR 12-FEB-1999; 99US-0119906P.
XX PR 18-NOV-1999; 99US-0166271P.
XX PA (AMGE-) AMGEN INC.
XX PI Boyle WJ, Hsu H;
XX WPI; 2000-558217/51.
XX PT Novel polypeptides comprising tumor necrosis factor ligand family
PT proteins, useful for treating inflammatory and immune disorders, e.g.
PT rheumatoid arthritis.
XX PS Claim 14; Fig 9; 71pp; English.
XX CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand family
CC member. AGP-3 is a type II transmembrane protein, and is a potent B cell
CC stimulatory factor. Expression of AGP-3 correlates to increases in the
CC number of B cells and immunoglobulins produced. AGP-3 proteins,
CC antibodies, and nucleic acids may be used to treat inflammatory and
CC immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and
CC graft versus host disease. The nucleic acids may be used to regulate the
CC expression of an AGP-3 related protein. The AGP-3 proteins, antibodies
CC and nucleic acids are also useful for the detection of AGP-3 agonists,
CC antagonists and characterizing interactions with AGP-3 related proteins
XX Sequence 172 AA;
SQ

Query Match 49.2%; Score 633; DB 3; Length 172;
Best Local Similarity 71.4%; Pred. No. 1.3e-53;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

QY 81 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLNGLVTH 140

Db 4 POKVAHITGIRTSNSALPISKDKTLGQKIESWESSRKGHSFLNHLVPLNGELVIEQ 63
141 KGFYIYISOTYFRFQEE-----IKENTKNDKOMVOYIKYTSYDPDILLMKSRNSCWS 194
Db 64 EGLYIYISOTYFRFQEAEDASRWSKDKVTKQLVQYIYKTSYDPDPIVLMKSRNSCWS 123
QY 195 KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
Db 124 RDAEYGLYSIYQGGIFELKKNDRIFVSVTNEHLMDLDQASFFGAFLI 171

RESULT 15

AAG03752
ID AAG03752 standard; protein; 121 AA.

XX AC AAG03752;

XX DT 06-OCT-2000 (first entry)

XX DE Human secreted protein, SEQ ID NO: 7833.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KN gene therapy; chromosome mapping.

XX OS Homo sapiens.

XX FN BP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-00200610.

XX PR 26-FEB-1999; 99US-0122487P.

XX PA (GBST) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX DR WPI; 2000-500381/45.

XX DR N-PSDB; AAC03758.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX PS Claim 13; SEQ ID NO 7833; 71pp + Sequence Listing; English.

XX CC The present sequence is a polypeptide encoded by one of a large number of
XX CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX CC tissues. EST sequences usually correspond mainly to the 3' untranslated
XX CC region (UTR) of the mRNA because they are often obtained from oligo-dT
XX CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX CC sequences derived from the 5' ends of mRNAs and even in those cases where
XX CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX CC are also used in diagnostic, forensic, gene therapy and chromosome
XX CC mapping procedures. They are used to obtain upstream regulatory sequences
XX CC and to design expression and secretion vectors

XX SQ Sequence 121 AA;

Query Match 33.0%; Score 425; DB 3; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.8e-33;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYNDPNDDEESNPFQVQKQLVLRKMLRTSEE 60

Db 39 TNELKQMDKYKSGIACFLKEDDSYNDPNDDEESNPFQVQKQLVLRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERG 80

Db 99 TISTVQEKQONISPLVRERG 118

Search completed: June 3, 2004, 09:02:57
Job time : 61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 09:04:27 ; Search time 47 Seconds
(without alignments)
1454.581 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELQMDKYSKSIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 715872

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PTC_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PTCUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887	68.9	168	9	US-09-900-530A-10
2	878	68.2	166	9	US-09-779-050A-16
3	859	66.7	164	13	US-10-116-378-29
4	850	66.0	161	14	US-10-216-074-7
5	849	66.0	161	14	US-10-338-083-11
6	826	64.2	288	9	US-09-855-544A-16
7	746.5	58.0	188	9	US-09-855-544A-14
8	636	49.4	172	9	US-09-779-050A-17
9	446	34.7	85	14	US-10-286-696-12
10	370	28.7	113	9	US-09-855-544A-15
11	291	22.6	98	9	US-09-855-544A-10
12	291	22.6	101	12	US-10-652-244-4
13	278	21.6	56	15	US-10-399-018-20
14	277	21.5	88	9	US-09-855-544A-9
15	245.5	19.1	87	14	US-10-286-696-13

16	236	18.3	178	15	US-10-338-785A-2	Sequence 2, Appli
17	233.5	18.1	199	12	US-10-289-456-86	Sequence 86, Appl
18	233.5	18.1	199	14	US-10-050-902-224	Sequence 224, App
19	233.5	18.1	199	14	US-10-050-898-224	Sequence 224, App
20	232.5	18.1	151	14	US-10-338-083-10	Sequence 10, Appl
21	232.5	18.1	158	12	US-10-289-456-101	Sequence 101, Appl
22	232.5	18.1	159	12	US-10-289-456-84	Sequence 84, Appl
23	232.5	18.1	160	9	US-09-779-050A-15	Sequence 15, Appl
24	232.5	18.1	165	12	US-10-289-456-103	Sequence 103, App
25	232.5	18.1	178	12	US-10-289-456-83	Sequence 83, Appl
26	232.5	18.1	180	12	US-10-289-456-100	Sequence 100, App
27	232.5	18.1	185	14	US-10-050-902-320	Sequence 320, App
28	232.5	18.1	185	14	US-10-050-898-320	Sequence 320, App
29	232.5	18.1	187	12	US-10-289-456-102	Sequence 102, App
30	230.5	17.9	170	10	US-09-791-153A-76	Sequence 76, Appl
31	230.5	17.9	193	12	US-10-289-456-96	Sequence 96, Appl
32	228.5	17.8	160	9	US-09-779-050A-14	Sequence 14, Appl
33	228.5	17.8	170	12	US-10-289-456-99	Sequence 99, Appl
34	190.5	14.8	213	14	US-10-185-425-2	Sequence 2, Appli
35	184.5	14.3	213	14	US-10-185-425-3	Sequence 3, Appli
36	177	13.8	159	14	US-10-185-425-1	Sequence 1, Appli
37	175.5	13.6	149	9	US-09-934-465-17	Sequence 17, Appl
38	175	13.6	34	14	US-10-272-411-24	Sequence 24, Appl
39	175	13.6	34	14	US-10-272-328A-24	Sequence 8, Appli
40	175	13.6	143	9	US-09-779-050A-8	Sequence 8, Appli
41	175	13.6	152	14	US-10-170-812-8	Sequence 5, Appli
42	173	13.4	138	14	US-10-216-074-5	Sequence 3, Appli
43	173	13.4	138	14	US-10-338-083-3	Sequence 30, Appl
44	173	13.4	140	13	US-10-116-378-30	Sequence 22, Appl
45	173	13.4	141	9	US-09-877-156-22	

ALIGNMENTS

RESULT 1
US-09-900-530A-10
; Sequence 10, Application US/09900530A
; Patent No. US20020128438A1
; GENERAL INFORMATION:
; APPLICANT: Seol, Dae-Wu
; APPLICANT: Billiar, Timothy R.
; TITLE OF INVENTION: DNA Cassette for the Production of
; Secretable Recombinant Trimeric Trail Proteins, Tetracycline
; TITLE OF INVENTION: /doxycycline-inducible Adeno-Associated Virus Vector, Their
; TITLE OF INVENTION: Combination and Use in Gene Therapy
; FILE REFERENCE: 5006-1-002
; CURRENT APPLICATION NUMBER: US/09/900,530A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: KR 2000-38441
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 168
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-900-530A-10

Query Match	68.9%	Score	887	DB	9	Length	168
Best Local Similarity	100.0%	Pred. No.	3.1e-77				
Matches	168	Conservative	0	Mismatches	0	Gaps	0
Qy	76	VREGPQVAHIITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRANGE	135				
Db	1	VREGPQVAHIITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRANGE	60				
Qy	136	LVIHEKGPYYISQTYFRFOEIKENTKNDQKQVQYIKYTSYDDPILLMKASRNSCSWK	195				
Db	61	LVIHEKGPYYISQTYFRFOEIKENTKNDQKQVQYIKYTSYDDPILLMKASRNSCSWK	120				
Qy	196	DAEYGLISYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG	243				

Db 121 DAEGYGLSYIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 169

RESULT 2

US-09-779-050A-16

; Sequence 16, Application US/09779050A

; Patent No. US20020160416A1

; GENERAL INFORMATION:

; APPLICANT: BOYLE, WILLIAM

; APPLICANT: HSU, HAILING

; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY

; FILE REFERENCE: A-570B

; CURRENT APPLICATION NUMBER: US/09/779,050A

; CURRENT FILING DATE: 2001-02-12

; PRIOR APPLICATION NUMBER: 60/181,800

; PRIOR FILING DATE: 2000-02-11

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 16

; LENGTH: 166

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-779-050A-16

Query Match 68.2%; Score 878; DB 9; Length 166;

Best Local Similarity 100.0%; Pred. No. 2.2e-76;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGPORVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 137

DB 1 ERGPORVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 60

QY 138 IHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 197

DB 61 IHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 198 EYGLSYIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 243

DB 121 EYGLSYIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 166

RESULT 3

US-10-116-378-29

; Sequence 29, Application US/10116378

; Publication No. US20020150993A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Marsters, Scot A.

; APPLICANT: Pitti, Robert M.

; APPLICANT: Wood, William

; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND

; TITLE OF INVENTION: NUCLEIC

; FILE REFERENCE: P1206R1

; CURRENT APPLICATION NUMBER: US/10/116,378

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09

; NUMBER OF SEQ ID NOS: 31

; SEQ ID NO 29

; LENGTH: 164

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-116-378-29

Query Match 66.7%; Score 859; DB 13; Length 164;

Best Local Similarity 99.4%; Pred. No. 1.5e-74;

Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 80 GPORVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 139

DB 1 GPORVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 60

QY 140 EKGFIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 199

DB 61 EKGFIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 200 GLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 243

DB 121 GLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 164

RESULT 4

US-10-216-074-7

; Sequence 7, Application US/10216074

; Publication No. US20030148445A1

; GENERAL INFORMATION:

; APPLICANT: Shu, Hong-Bing

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/10/216,074

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US/09/565,423

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 7

; LENGTH: 161

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-216-074-7

Query Match 66.0%; Score 850; DB 14; Length 161;

Best Local Similarity 100.0%; Pred. No. 1.1e-73;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 142

DB 1 RVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 60

QY 143 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 202

DB 61 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 243

DB 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 161

RESULT 5

US-10-338-083-11

; Sequence 11, Application US/10338083

; Publication No. US20030166559A1

; GENERAL INFORMATION:

; APPLICANT: Desjarlais, John R.

; APPLICANT: Tansey, Malu Lourdes G.

; APPLICANT: Dahiyat, Bassil I.

; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof

; FILE REFERENCE: A-71273-2

; CURRENT APPLICATION NUMBER: US/10/338,083

; CURRENT FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/345,805

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: US 60/373,453

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patent in version 3.2

QY 80 GPORVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 139

DB 1 GPORVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 60

QY 140 EKGFIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 199

DB 61 EKGFIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 200 GLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 243

DB 121 GLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 164

RESULT 4

US-10-216-074-7

; Sequence 7, Application US/10216074

; Publication No. US20030148445A1

; GENERAL INFORMATION:

; APPLICANT: Shu, Hong-Bing

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/10/216,074

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US/09/565,423

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 7

; LENGTH: 161

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-216-074-7

Query Match 66.0%; Score 850; DB 14; Length 161;

Best Local Similarity 100.0%; Pred. No. 1.1e-73;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 142

DB 1 RVAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELV 60

QY 143 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 202

DB 61 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 243

DB 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 161

RESULT 5

US-10-338-083-11

; Sequence 11, Application US/10338083

; Publication No. US20030166559A1

; GENERAL INFORMATION:

; APPLICANT: Desjarlais, John R.

; APPLICANT: Tansey, Malu Lourdes G.

; APPLICANT: Dahiyat, Bassil I.

; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof

; FILE REFERENCE: A-71273-2

; CURRENT APPLICATION NUMBER: US/10/338,083

; CURRENT FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/345,805

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: US 60/373,453

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patent in version 3.2

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; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match      66.0%; Score 849; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 ORVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEH 141
DB 1 QVAAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEH 60

QY 142 GFYIYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDPDILLMKSARNSCWSKDAEYGL 201
DB 61 GFYIYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDPDILLMKSARNSCWSKDAEYGL 120

QY 202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLV 242
DB 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLV 161

RESULT 6
US-09-855-544A-15
; Sequence 16, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match      64.2%; Score 826; DB 9; Length 208;
Best Local Similarity 96.3%; Pred. No. 3.1e-71;
Matches 156; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIEHKGFIYYSQTYFRFQBEIKENT 162
DB 159 SGHSFLSNLHRLNGELVIEHKGFIYYSQTYFRFQBEIKENT 200

RESULT 7
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-14

Query Match      58.0%; Score 746.5; DB 9; Length 188;
Best Local Similarity 61.7%; Pred. No. 1.2e-63;
Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSR 104

QY 121 SGHSFLSNLHRLNGELVIEHKGFIYYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDP 180
DB 105 -----ENTKNDKQVYIYKYTSYDP 125

QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAP 240
DB 126 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAP 185

QY 241 LVG 243
DB 186 LVG 188

RESULT 8
US-09-779-050A-17
; Sequence 17, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-17

Query Match      49.4%; Score 636; DB 9; Length 172;
Best Local Similarity 71.4%; Pred. No. 4.6e-53;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

QY 81 PORVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEH 140
DB 4 PORVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEH 63

QY 141 KGFIYYSQTYFRFQBEI-----IKENTKNDKQVYIYKYTSYDPDILLMKSARNSCWS 194
DB 64 EGLYIYSQTYFRFQBEADASKMVKDKVTKQLVQIYKYTSYDPDILLMKSARNSCWS 123

QY 195 KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLV 242
DB 124 RDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLV 171

RESULT 9
US-10-286-696-12
; Sequence 12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
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Db 64 E---YIYSQTYERFQE 76

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OM protein - protein search, using sw model

Run on: June 3, 2004, 09:01:51 ; Search time 22 Seconds
(without alignments)
570.232 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKQMDKYSGIACFL.....NEHLIDMDHESFFGAFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 317993

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	72.3	177	3	US-09-105-343A-7
2	850	66.0	161	4	US-09-585-423-7
3	654	50.8	183	3	US-09-105-343A-8
4	446	34.7	85	4	US-09-632-287A-12
5	291	22.6	101	1	US-08-670-354-4
6	291	22.6	101	3	US-09-320-424-4
7	291	22.6	101	4	US-09-825-563-4
8	291	22.6	101	5	PCT-US96-10895-4
9	245.5	19.1	87	4	US-09-632-287A-13
10	228.5	17.8	173	4	US-09-396-937-10
11	228.5	17.8	173	4	US-09-396-937-12
12	228.5	17.8	187	4	US-09-396-937-8
13	210	16.3	182	4	US-09-396-937-16
14	208	16.2	188	4	US-09-396-937-14
15	202.5	15.7	173	4	US-09-396-937-20
16	195.5	15.2	173	4	US-09-396-937-18
17	189.5	14.7	179	4	US-08-339-214-22
18	182	14.1	138	4	US-08-339-214-20
19	181.5	14.1	178	4	US-08-339-214-84
20	181.5	14.1	179	3	US-08-649-100-9
21	181.5	14.1	179	4	US-08-339-214-6
22	179	13.9	137	4	US-08-339-214-18
23	178	13.8	145	3	US-08-630-172-5
24	178	13.8	145	3	US-09-375-419-5
25	177.5	13.8	179	4	US-08-339-214-14
26	175.5	13.6	149	3	US-08-584-031-17
27	175	13.6	152	4	US-09-496-118B-8

Sequence 4, Appli
Sequence 12, Appli
Sequence 81, Appli
Sequence 5, Appli
Sequence 80, Appli
Sequence 4, Appli
Sequence 22, Appli
Sequence 79, Appli
Sequence 83, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 82, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 39, Appli

28 173 13.4 138 4 US-08-339-214-4
29 173 13.4 138 4 US-08-339-214-12
30 173 13.4 138 4 US-08-339-214-81
31 173 13.4 138 4 US-09-565-423-5
32 173 13.4 139 4 US-08-339-214-80
33 173 13.4 139 4 US-08-968-686-4
34 173 13.4 141 3 US-09-286-629-22
35 173 13.4 141 4 US-08-339-214-79
36 170 13.2 136 4 US-08-339-214-83
37 170 13.2 136 4 US-08-968-686-8
38 170 13.2 137 4 US-08-339-214-2
39 170 13.2 137 4 US-08-339-214-10
40 170 13.2 137 4 US-08-339-214-82
41 161.5 12.5 240 3 US-08-913-014A-1
42 161.5 12.5 240 4 US-09-072-993C-4
43 161.5 12.5 240 4 US-09-653-285-1
44 160 12.4 174 4 US-09-131-237C-2
45 159.5 12.4 208 4 US-09-027-287-39

ALIGNMENTS

RESULT 1
US-09-105-343A-7
; Sequence 7, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-7

Query Match 72.3%; Score 930; DB 3; Length 177;
Best Local Similarity 99.4%; Pred. No. 1.2e-88;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 67 EKOQNSPLVREGPORVAAHITGTGRNTLSSPNSKNEKALGRKINSWESSRSCHSFL 126

Db 1 EKQONISPLVRERGQORVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRGHSFL 60
QY 127 SNLHRLNGELVTHEKGFYIYSQTYFRQBEIKENTKNDKQKQVYIYKTSYDPPIILMK 186
Db 61 SNLHRLNGELVTHEKGFYIYSQTYFRQBEIKENTKNDKQKQVYIYKTSYDPPIILMK 120
QY 187 SARNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLVG 243
Db 121 SARNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLVG 177

RESULT 2

US-09-565-423-7
; Sequence 7, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-7

Query Match 66.0%; Score 850; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.1e-80;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRGHSFLSNLHRLNGELVTHEK 142
Db 1 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRGHSFLSNLHRLNGELVTHEK 60
QY 143 FYIYSQTYFRQBEIKENTKNDKQKQVYIYKTSYDPPIILMKSAARNCSWSDAEYGLY 202
Db 61 FYIYSQTYFRQBEIKENTKNDKQKQVYIYKTSYDPPIILMKSAARNCSWSDAEYGLY 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLVG 161

RESULT 3

US-09-105-343A-8
; Sequence 8, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Fast-SEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-8
Query Match 50.8%; Score 654; DB 3; Length 183;
Best Local Similarity 68.7%; Pred. No. 5.6e-60;
Matches 125; Conservative 22; Mismatches 29; Indels 6; Gaps 1;
QY 67 EKQONISPLVRERGQORVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRGHSFL 126
Db 1 EKQSTPPLPRGGRPQKVAAHITGTRRSNSALIPISKDGTGLGKIESWESSRGHSFL 60
QY 127 SNLHRLNGELVTHEKGFYIYSQTYFRQBEI-----IKENTKNDKQKQVYIYKTSYDP 180
Db 61 NHVLFNGELVTHEKGFYIYSQTYFRQBEADASKVSKQVTKQLVQIYIYKTSYDP 120
QY 181 PILLMKSAARNCSWSDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAP 240
Db 121 PIVLAKSAARNCSWSDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDLDOEASFFGAP 180
QY 241 LV 242
Db 181 II 182

RESULT 4

US-09-632-287A-12
; Sequence 12, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott X
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; PRIOR FILING DATE: 2000-08-03/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-632-287A-12

Query Match 34.7%; Score 446; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 7.1e-39;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 ERQPRVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRGHSFLSNLHRLNGELV 137

Db 1 ERGPORVAHITGRGNTLSGPNKNEKALGRKINSWESSRSGHFLSNLHLRNGELV 60
Qy 138 IHEKGFYIYSQYFRQBEIKENT 162
Db 61 IHEKGFYIYSQYFRQBEIKENT 85

RESULT 5
US-08-670-354-4
; Sequence 4, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-4

Query Match 22.6%; Score 291; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQKWLRLVRK 52
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQKWLRLVRK 90

RESULT 6
US-09-320-424-4
; Sequence 4, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis

; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-09-320-424-4

Query Match 22.6%; Score 291; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQKWLRLVRK 52
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQKWLRLVRK 90

RESULT 7
US-09-825-563-4
; Sequence 4, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-09-825-563-4

Query Match 22.6%; Score 291; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQKWLRLVRK 52
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQKWLRLVRK 90

RESULT 8
PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895


```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPG, residues 158-316 with C to S
; OTHER INFORMATION: mutation, and His tag
US-09-396-937-12

Query Match      17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred. No. 7.4e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFY 145
Db 22 AHLT-----INAAISPGSHKVTL---SSWYHDR-GWAKISNMTLSNGKLRVNDGFFY 71
QY 146 IYSQTYFRQBEIKENTKNDKQMVQYIKYT-SYEDPILLMKSARNSCWSDAEVGLYSI 204
Db 72 LYANICFRHETSGSVPTDYQLQVMVYVKTSIKIPSSNHLMKGGSTKQWNSGNSEPHFYSI 131
QY 205 YOGGIPFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 132 NVGGPFKLAGEISIQVSNPSLLDPDQDATYFGAFV 169

RESULT 12
US-09-396-937-8
; Sequence 8, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR
; OTHER INFORMATION: product with optimum codons for E. coli and P.
; OTHER INFORMATION: pastoris expression
US-09-396-937-8

Query Match      17.8%; Score 228.5; DB 4; Length 187;
Best Local Similarity 34.2%; Pred. No. 8.3e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFY 145
Db 36 AHLT-----INAAISPGSHKVTL---SSWYHDR-GWAKISNMTLSNGKLRVNDGFFY 85
QY 146 IYSQTYFRQBEIKENTKNDKQMVQYIKYT-SYEDPILLMKSARNSCWSDAEVGLYSI 204
Db 86 LYANICFRHETSGSVPTDYQLQVMVYVKTSIKIPSSNHLMKGGSTKQWNSGNSEPHFYSI 145
QY 205 YOGGIPFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 146 NVGGPFKLAGEISIQVSNPSLLDPDQDATYFGAFV 183

RESULT 13
US-09-396-937-16
; Sequence 16, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
```

```
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: between murine OPG, residues 158-316 with tetanus
; OTHER INFORMATION: toxoid P2 epitope introduced, and His tag
US-09-396-937-16

Query Match      16.3%; Score 210; DB 4; Length 182;
Best Local Similarity 32.0%; Pred. No. 6.6e-14;
Matches 55; Conservative 31; Mismatches 56; Indels 30; Gaps 6;

QY 86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFY 145
Db 22 AHLT-----INAAISPGSHKVTL---SSWYHDR-GWAKISNMTLSNGKLRVNDGFFY 71
QY 146 IYSQTYFRQBEIKENTKNDKQMVQYIKYTSPDPILLMKS-----ARNS----- 191
Db 72 LYANICFRHETSGSVPTDYQLQVMVYVK-----TIKQSSNHLNQYIKANSKFICITE 126
QY 192 -CWSKDAEYGLYSIYOGGIPFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 127 LNWGNSSEPHFYSINGVGGFFKLAGEISIQVSNPSLLDPDQDATYFGAFV 178

RESULT 14
US-09-396-937-14
; Sequence 14, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPG, residues 158-316 modified by
; OTHER INFORMATION: introduction of tetanus toxoid P30 epitope, and
; OTHER INFORMATION: His tag
US-09-396-937-14

Query Match      16.2%; Score 208; DB 4; Length 188;
Best Local Similarity 30.5%; Pred. No. 1.1e-13;
Matches 53; Conservative 34; Mismatches 59; Indels 28; Gaps 5;

QY 86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFY 145
Db 22 AHLT-----INAAISPGSHKVTL---SSWYHDR-GWAKISNMTLSNGKLRVNDGFFY 71
QY 146 IYSQTYFRQBEIKENTKNDKQMVQYIKYTSPDP-----ILMKSA 188
Db 72 LYANICFRHETSGSVPTDYQLQVMVYVK-TSIIKIPSSNHLMFNFTVSWFLVAPKVAS 130
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QY 189 RNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 131 HLENWGNSEHFYFYSINVGGFFKLAGEEISIQVSNPSLLDPDQDATYFGAFV 184

RESULT 15

US-09-396-937-20
; Sequence 20, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC.1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion between
; OTHER INFORMATION: murine OPG, residues 158-316 with tetanus toxoid
; OTHER INFORMATION: P30 epitope introduced, and His tag
US-09-396-937-20

Query Match 15.7%; Score 202.5; DB 4; Length 173;
Best Local Similarity 30.2%; Pred. No. 3.7e-13;
Matches 52; Conservative 28; Mismatches 53; Indels 39; Gaps 5;
QY 86 AHITGRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFY 145
Db 22 AHLT-----INAAISFGSHKVTL---SSWYHDR-GWAKISMTLSNGKLAVNQDGFY 71
QY 146 IYQTYFR-----FQEEIKENTKDKQVQYIKYTSYPPDILLMKARN 190
Db 72 LYANICFNFTVSWFLRVPKVSASHLEVKTISK-----IPSSENLMKGGST 117
QY 191 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 118 KWSGNSSEHFYFYSINVGGFFKLAGEEISIQVSNPSLLDPDQDATYFGAFV 169

Search completed: June 3, 2004, 09:05:32
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 11:26:36 ; Search time 60 Seconds
(without alignments)
1144.317 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKQMDKYSGKIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep 29Jan04 : *
1: Genesep1980s : *
2: Genesep1990s : *
3: Genesep2000s : *
4: Genesep2001s : *
5: Genesep2002s : *
6: Genesep2003as : *
7: Genesep2003bs : *
8: Genesep2004s : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	279	2 AAW76332	AAW76332 Human TL2
2	1287	100.0	279	2 AAW95032	AAW95032 Tumour ne
3	1287	100.0	281	2 AAW19777	AAW19777 Novel cyt
4	1287	100.0	281	2 AAW27134	AAW27134 Human Apo
5	1287	100.0	281	2 AAW19787	AAW19787 Human Apo
6	1287	100.0	281	2 AAW76829	AAW76829 Human TL2
7	1287	100.0	281	2 AAW56760	AAW56760 Human TRA
8	1287	100.0	281	2 AAW44354	AAW44354 Human AGP
9	1287	100.0	281	2 AAY01517	AAY01517 Protein a
10	1287	100.0	281	2 AAY27012	AAY27012 Human Apo
11	1287	100.0	281	3 AAY81956	AAY81956 Human Apo
12	1287	100.0	281	3 AAB24038	AAB24038 Human PRO
13	1287	100.0	281	3 AAB08545	AAB08545 Amino aci
14	1287	100.0	281	3 AAB28691	AAB28691 Human AGP
15	1287	100.0	281	4 AAB50977	AAB50977 Human PRO
16	1287	100.0	281	4 AAB67243	AAB67243 Human Apo
17	1287	100.0	281	4 AAE11031	AAE11031 Human TNF
18	1287	100.0	281	4 AAB48350	AAB48350 Human TL2
19	1287	100.0	281	5 ABB08133	ABB08133 Human TRA
20	1287	100.0	281	5 ABG31630	ABG31630 Human TRA
21	1287	100.0	281	5 AAU75062	AAU75062 Human TNF
22	1287	100.0	281	5 AAM51077	AAM51077 Human Apo
23	1287	100.0	281	5 ABP51954	ABP51954 Human Apo
24	1287	100.0	281	5 AAO19095	AAO19095 C neofom
25	1287	100.0	281	5 AAU79593	AAU79593 Human TNF

26	1287	100.0	281	6 ABG73861	ABG73861 Human Apo
27	1287	100.0	281	6 ABU10205	ABU10205 Human Apo
28	1287	100.0	281	6 ABU71443	ABU71443 Human neo
29	1287	100.0	281	6 ABG72738	ABG72738 Human TNF
30	1287	100.0	281	6 AAO29543	AAO29543 Human TRA
31	1287	100.0	281	6 ABU08558	ABU08558 Human TNF
32	1287	100.0	281	6 ABR42313	ABR42313 Human TRA
33	1287	100.0	281	6 ABG71905	ABG71905 Human TRA
34	1287	100.0	281	6 ABP60546	ABP60546 Human tum
35	1287	100.0	281	6 AAB36258	AAB36258 Human TR4
36	1287	100.0	281	6 AAO31151	AAO31151 Human TNF
37	1287	100.0	281	6 ABO25125	ABO25125 Human TNF
38	1287	100.0	281	7 AD861471	AD861471 Native hu
39	1287	100.0	281	7 ADC35202	ADC35202 Human TNF
40	1287	100.0	281	7 ADD14080	ADD14080 Human SRC
41	1287	100.0	281	7 ADD19010	ADD19010 Human dis
42	1287	100.0	281	8 AD876953	AD876953 Human pro
43	1284	99.8	281	7 AD861488	AD861488 Human Apo
44	1282	99.6	266	4 AAY72935	AAY72935 OmpA sign
45	1282	99.6	281	5 ABG72257	ABG72257 Human tum

ALIGNMENTS

RESULT 1
AAW76332
ID AAW76332 standard; protein; 279 AA.
XX
AC AAW76332;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human TL2 (TRAIL), ligand for TR5.
XX
KW TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation;
KW arthritis; septicaemia; transplant rejection; autoimmune disease;
KW inflammatory bowel disease; graft versus host disease; infection; stroke;
KW ischaemia; acute respiratory disease syndrome; psoriasis; restenosis;
KW brain injury; AIDS; bone disease; cancer; atherosclerosis;
KW Alzheimer's disease; human; therapy; diagnosis; ligand.
XX
OS Homo sapiens.
XX
PN EP867509-A2.
XX
PD 30-SEP-1998.
XX
PF 04-FEB-1998; 98EP-00300827.
XX
PR 05-FEB-1997; 97US-00795910.
XX
PR 28-JUL-1997; 97US-00901469.
XX
PA (SMK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR, Tan KB, Truneh A, Lyn SDP;
XX
XX WPI; 1998-497862/43.
XX
XX New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent
XX and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases,
XX infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,
XX AIDS and bone diseases.
XX
XX Disclosure; Page 17-18; 22pp; English.
XX
XX This is the amino acid sequence of human TL2 (also known as TRAIL), which
XX has newly been discovered to be a ligand of human tumour necrosis related
XX receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and
XX TL2 can be used in screening processes for compounds which bind the
XX receptor, or its ligand, and which activate (agonists) or inhibit
XX (antagonists) the receptor or TL2. Treatment of a subject with the need
XX to inhibit TR5 polypeptide activity comprises administering an antagonist

CC to the polypeptide, administering a nucleic acid that inhibits the
 CC expression of the nucleotide sequence encoding the polypeptide and/or
 CC administering a polypeptide that competes with the polypeptide for its
 CC ligand, substrate or receptor. The active agents can be used for the
 CC treatment of chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),
 CC transplant rejection, graft vs host disease, infection, stroke,
 CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,
 CC AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),
 CC atherosclerosis and Alzheimer's disease
 XX
 SQ Sequence 279 AA;

Query Match 100.0%; Score 1287; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESNMSPCWQVQWQLRQVLRKMLRTSEE 60
 DB 37 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESNMSPCWQVQWQLRQVLRKMLRTSEE 96
 QY 61 TISTVQEKQNISPLVREGRGPQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 120
 DB 97 TISTVQEKQNISPLVREGRGPQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 156
 QY 121 SGHSFSLNHLRNGELVIEHKGFPYIYSQTYRFOEIKENTKNDKQWQVIYKYTSYPD 180
 DB 157 SGHSFSLNHLRNGELVIEHKGFPYIYSQTYRFOEIKENTKNDKQWQVIYKYTSYPD 216
 QY 181 PILLMKSARNCSWCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 217 PILLMKSARNCSWCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
 QY 241 LVG 243
 DB 277 LVG 279

RESULT 2
 AAW95032
 ID AAW95032 standard; protein; 279 AA.

XX AAW95032;

DT 13-MAY-1999 (first entry)

XX Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.

XX Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
 XX inflammation; septicemia; autoimmune disease, transplant rejection;
 XX graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
 XX acute respiratory disease syndrome; restenosis; bone disease; cancer;
 XX atherosclerosis; Alzheimer's disease.

XX Unidentified.

XX EP897114-A2.

XX 17-FEB-1999.

XX 04-JUN-1998; 98EP-00304424.

XX 13-AUG-1997; 97US-0055513P.

XX 26-AUG-1997; 97US-0056980P.

XX 29-AUG-1997; 97US-0057550P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Brigham-Burke MR, Young PR;

XX WPI; 1999-134308/12.

XX Identifying agonists and antagonists to tumour necrosis factor receptor

PT (TNF-R) related polypeptides (LR1, LR2, LR2 and LR4) - useful for
 PT treating stroke, Alzheimer's disease and AIDS.
 XX
 PS Disclosure; Page 14-15; 18pp; English.

XX The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
 CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
 CC assessing the ability of the candidate compound to compete with TR1 or
 CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
 CC for treating diseases caused by imbalance of TL or TR polypeptide levels,
 CC which cause chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases, transplant rejection, graft vs. host disease,
 CC infection, stroke, ischemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and
 CC Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TL2
 XX
 SQ Sequence 279 AA;

Query Match 100.0%; Score 1287; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESNMSPCWQVQWQLRQVLRKMLRTSEE 60
 DB 37 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESNMSPCWQVQWQLRQVLRKMLRTSEE 96
 QY 61 TISTVQEKQNISPLVREGRGPQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 120
 DB 97 TISTVQEKQNISPLVREGRGPQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 156
 QY 121 SGHSFSLNHLRNGELVIEHKGFPYIYSQTYRFOEIKENTKNDKQWQVIYKYTSYPD 180
 DB 157 SGHSFSLNHLRNGELVIEHKGFPYIYSQTYRFOEIKENTKNDKQWQVIYKYTSYPD 216
 QY 181 PILLMKSARNCSWCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 217 PILLMKSARNCSWCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
 QY 241 LVG 243
 DB 277 LVG 279

RESULT 3
 AAW19777

ID AAW19777 standard; protein; 281 AA.

XX AAW19777;

DT 22-SEP-1997 (first entry)

XX Novel cytokine Apo-2 ligand.

XX Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..281 /note= "Claim 4"

FT Region 1..14 /label= Cytoplasmic_region

FT Protein 15..281 /note= "Claim 3"

FT Region 15..40 /label= Transmembrane_region

FT Protein 41..281 /note= "Claim 2"

FT Region 41..281

FT Modified-site /label= Extracellular_region
 FT 109
 FT /label= Glycosylation
 FT /note= "putative N-linked glycosylation site"
 FT 114. .281
 FT Protein /note= "Claim 1"
 FT XX
 FT XX
 PN WO9725428-A1.
 XX
 XX 17-JUL-1997.
 PD
 XX 08-JAN-1997; 97WO-US000272.
 PF
 XX 09-JAN-1996; 96US-00584031.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Chuntharapai A, Kim KJ;
 PI WPI; 1997-372867/34.
 XX N-PSDB; AAT72796.
 DR
 XX Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
 PT apoptosis for the treatment of breast and colon cancer.
 FT
 XX Claim 4; Fig 1a; 72pp; English.
 PS
 XX A novel cytokine (AAW1977), designated Apo-2 ligand, induces mammalian
 CC cell apoptosis. It is believed to be a member of the tumour necrosis
 CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
 CC clone (AA72796) isolated from a human placental cDNA library. Apo-2
 CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
 CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
 CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
 CC acid. They can be used to induce apoptosis in mammals and to treat
 CC pathological conditions such as cancer (esp. breast or colon cancer) or
 CC to raise antibodies useful in diagnostic assays
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQVLRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQVLRKMLRTSEE 98
 QY 61 TISTVQEKQNTISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNTISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHLNGLVIRHEKGFYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDP 180
 DB 159 SGHSFLSNLHLNGLVIRHEKGFYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDP 218
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281
 RESULT 4
 AAW27134
 ID AAW27134 standard; protein; 281 AA.
 XX
 XX AAW27134;
 XX
 DT 02-APR-1998 (first entry)
 XX

DE Human Apoptosis inducing molecule-I (AIM-I).
 XX
 KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
 KW tumour necrosis factor ligand superfamily; AIM-I altered expression;
 KW neoplasia inhibition; anti-inflammatory agent.
 XX
 OS Homo sapiens.
 XX
 PN WO9733899-A1.
 XX
 XX 18-SEP-1997.
 PD
 XX 14-MAR-1996; 96WO-US003773.
 PF
 XX 14-MAR-1996; 96WO-US003773.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM;
 PI WPI; 1997-470807/43.
 XX N-PSDB; AAT85210.
 DR
 XX New isolated apoptosis inducing molecule-I - used to develop products for
 PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
 FT versus host disease or inflammation.
 XX
 XX Claim 2; Fig 1; 82pp; English.
 PS
 XX The present sequence represents a human Apoptosis inducing molecule-I
 CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand of
 CC superfamily. The products can be used in the diagnosis and treatment of
 CC disorders related to under-expression, over-expression or altered
 CC expression of AIM-I. AIM-I or agonists can be used for treating
 CC autoimmune disorders including systemic lupus erythematosus,
 CC immunoproliferative disease lymphadenopathy (IPL),
 CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
 CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
 CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
 CC haematopoiesis in endothelial cell development, to stimulate peripheral
 CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
 CC osteoporosis, for preventing graft-host rejection, and as anti-
 CC inflammatory agents, for treating endotoxemic shock or to prevent
 CC activation of HIV
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQVLRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQVLRKMLRTSEE 98
 QY 61 TISTVQEKQNTISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNTISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHLNGLVIRHEKGFYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDP 180
 DB 159 SGHSFLSNLHLNGLVIRHEKGFYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDP 218
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

```
RESULT 5
AAW19787
ID AAW19787 standard; protein; 281 AA.
XX
AC AAW19787;
XX
CC 24-SEP-1997 (first entry)
XX
DT Human apoptosis inducer cytokine TRAIL.
XX
DE Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
XX cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
XX thrombotic microangioplasty; therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Domain Location/Qualifiers
FT 1..18 /label= Cytoplasmic_domain
FT 19..38 /label= Transmembrane_domain
FT 39..281 /label= Extracellular_domain
FT /note= "contains a receptor-binding region"
FT Cleavage-site 39..90 /note= "potential KEX2 protease processing site"
FT Modified-site 109..111 /note= "potential N-glycosylation site"
FT Cleavage-site 149..150 /note= "potential KEX2 protease processing site"
XX
XX WC9701633-AL.
XX
XX 16-JAN-1997.
XX
XX 25-JUN-1996; 96WO-US010895.
XX
XX 29-JUN-1995; 95US-00496632.
XX 01-NOV-1995; 95US-00548368.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Wiley SR, Goodwin RG;
XX WPI; 1997-118715/11.
XX N-PSDB; AAW72847.
XX
XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
XX cells - useful for treating thrombotic microangiopathy, cancer and viral
XX infection and for use in assays.
XX
XX Claim 10; Page 43-44; 62pp; English.
XX
XX Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
XX (AAW19787) is a novel cytokine that induces apoptosis of certain target
XX cells, including cancer cells and virally infected cells. Its amino acid
XX sequence was deduced from cDNA clone HuAIC (AAW72848), deposited in
XX vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
XX polypeptides) can be expressed in host cells and used in the treatment of
XX cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
XX to raise antibodies that may be useful for treating thrombotic
XX microangiopathies
XX
XX Sequence 281 AA;
XX
Query Match 100.0%; Score 1287; DB 2; Length 281;
Best Local Similarity 100.0%; Pred No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSGKIACFLKEDDSYWDNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKIACFLKEDDSYWDNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 98
```

```
QY 61 TISTVQEKQONISPLVREGRGPQVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVREGRGPQVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYPFQBEIKENTKNDKQMVQYIYKYTSYPD 180
DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYPFQBEIKENTKNDKQMVQYIYKYTSYPD 218
QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 6
AAW76829
ID AAW76829 standard; protein; 281 AA.
XX
AC AAW76829;
XX
DT 25-JAN-1999 (first entry)
XX
DE Human TL2 protein.
XX
DE TR6; tumour necrosis factor related receptor; human; treatment; stroke;
XX inflammation; arthritis; septicaemia; autoimmune disease; restenosis;
XX transplant rejection; infection; ischaemia; brain injury; bone disease;
XX acute respiratory disease syndrome; acquired autoimmune disease syndrome;
XX AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
XX TL2. tumour necrosis factor-related apoptosis-inducing ligand.
XX
OS Homo sapiens.
XX
XX EP870827-A2.
XX
XX 14-OCT-1998.
XX
XX 23-DEC-1997; 97EP-00310562.
XX
XX 14-MAR-1997; 97US-0041230P.
XX 09-MAY-1997; 97US-00853684.
XX 22-AUG-1997; 97US-00916625.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Deen KC, Young PR;
XX
XX WPI; 1998-523156/45.
XX N-PSDB; AAV63095.
XX
XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
XX polypeptide, antibody, agonist, antagonist, etc.
XX
XX Disclosure; Page 32-33; 34pp; English.
XX
XX This sequence represents the human tumour necrosis factor (TNF)-related
XX receptor TL2 (also known as tumour necrosis factor-related apoptosis-
XX inducing ligand, TRAIL). This protein is used in a method resulting in
XX the isolation of the novel human TNF related receptor, TR6. TR6
XX polypeptides and polynucleotides can be used in the treatment of chronic
XX and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g.
XX inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
XX host disease, infection, stroke, ischaemia, acute respiratory disease
XX syndrome, restenosis, brain injury, (acquired autoimmune disease
XX syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
XX disorders), atherosclerosis and Alzheimers disease
XX
XX Sequence 281 AA;
XX
Query Match 100.0%; Score 1287; DB 2; Length 281;
```

	Best Local Similarity	100.0%; Pred. No.	2.3e-117;	Matches	243; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY		1	TNELKQMCKYSKGSIACFLKEDDSYDNDPEESMNSPCWQVKQLRVKMILRTSEE	60					
Db		39	TNELKQMCKYSKGSIACFLKEDDSYDNDPEESMNSPCWQVKQLRVKMILRTSEE	98					
QY		61	TISTVQEKKQNISPLVRERGQRVAHHITGTRGSNTLSPNPKNEKALGRKINSWESSR	120					
Db		99	TISTVQEKKQNISPLVRERGQRVAHHITGTRGSNTLSPNPKNEKALGRKINSWESSR	158					
QY		121	SCHSFLSNLHRLNGELVTHEKGFYYIYSOTYFRFQBEIKENTKDQKVQYIYKYTSYPD	180					
Db		159	SCHSFLSNLHRLNGELVTHEKGFYYIYSOTYFRFQBEIKENTKDQKVQYIYKYTSYPD	218					
QY		181	PILLMKSRPNSCWSDAEBGYLSYQGIFELKENDRI FVSVTNEHLIDMDHEADSFFGAFA	240					
Db		219	PILLMKSRPNSCWSDAEBGYLSYQGIFELKENDRI FVSVTNEHLIDMDHEADSFFGAFA	278					
QY		241	LVG 243						
Db		279	LVG 281						
	RESULT 7								
	AANW56760								
ID	AANW56760 standard; protein; 281 AA.								
XX									
AC	AANW56760;								
DT	05-AUG-1998 (first entry)								
DE	Human TRAIL polypeptide.								
KX									
XW	Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;								
KW	Cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.								
OS	Homo sapiens.								
FH	Key								
FT	Domain	1..18	Location/Qualifiers						
FT	Region	/note= "N-terminal cytoplasmic domain"							
FT	Domain	39..281	/note= "transmembrane region"						
PN	US5763223-A.								
PD	09-JUN-1998.								
PP	25-JUN-1996;	96US-00670354.							
PR	29-JUN-1995;	95US-00496632.							
PR	01-NOV-1995;	95US-00548368.							
PA	(IMMV) IMMUNE CORP.								
PI	Goodwin RG, Wiley SR;								
PI	WPI; 1998-347322/30.								
DR	N-PSDB; AAV29518.								
XX	DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful								
PT	for producing recombinant polypeptides for research and therapy of								
PT	leukaemia, lymphoma, melanoma and viral infections.								
XX	Claim 1; Col 33-36; 28pp; English.								
XX	This represents a human tumour necrosis factor related apoptosis ligand								
CC	(TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce								
CC	apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful								
CC	for producing the recombinant TRAIL polypeptides, which may be useful in								

CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
CC haematopoietic diseases associated with reduction in the number of bone
CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
CC by disease, injury or exposure to myelosuppressive agents. Host cells,
CC transformed with expression vectors containing AGP-1 DNA, are used to
CC produce recombinant AGP-1
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESNMPCQVQKWLRLVVKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESNMPCQVQKWLRLVVKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 180
DB 159 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 218
QY 181 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 9

AAV01517
ID AAY01517 standard; peptide; 281 AA.

XX AAY01517;

XX 27-MAY-1999 (first entry)

XX Protein associated with neurodegenerative and autoimmune diseases.

XX Neurodegenerative disease; autoimmune disease; inflammatory disease;

XX lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;

XX surface receptor; TRAIL protein.

XX Homo sapiens.

XX FR2766713-A1.

XX 05-FEB-1999.

XX 04-AUG-1997; 97FR-00010176.

XX 04-AUG-1997; 97FR-00010176.

XX (INNR) BIO MERIEUX.

XX Rieger F, Belliveau JF, Perron H;

XX WPI; 1999-156177/14.

XX Use of polypeptide derived from TRAIL protein for diagnosis of
XX degenerative disease - autoimmunity and inflammation, also useful in
XX prevention or treatment, and similar use of corresponding ligand and
XX nucleic acid.

XX Claim 2; Page 13; 21pp; French.

XX The specification describes the use a polypeptide corresponding to at
XX least the primary sequence of part of the present sequence to produce a
XX diagnostic, prophylactic or therapeutic composition useful in cases of
XX degenerative, autoimmune and inflammatory diseases. The polypeptides can
XX be used in treatment of neurodegenerative diseases, lupus erythematosus,
XX rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
XX nervous system cells, antigenic and specifically recognise the surface
XX receptor of the TRAIL protein. The polypeptide is a marker of disease and
XX a therapeutic target, e.g. its apoptotic activity can be blocked with an
XX anti-TRAIL antibody or a TRAIL equivalent that binds to specific
XX receptors, inhibiting formation of natural complex

XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESNMPCQVQKWLRLVVKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESNMPCQVQKWLRLVVKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 180
DB 159 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 218
QY 181 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 10

AAV27012
ID AAY27012 standard; protein; 281 AA.

XX AAY27012;

XX 24-SEP-1999 (first entry)

XX Human Apo-2 ligand (Apo-2L) polypeptide.

XX Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
XX lupus; immune-mediated glomerular nephritis; human.

XX Homo sapiens.

XX WO9936535-A1.

XX 22-JUL-1999.

XX 15-JAN-1999; 99WO-US0001039.

XX 15-JAN-1998; 98US-00007886.

XX 15-APR-1998; 98US-00060533.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;

XX WPI; 1999-444397/37.

XX N-PSDB; AAX86987.

PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.
 XX
 PS Claim 1; Fig 1A; 86pp; English.
 XX
 CC This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDPDESMNSPCQVKQRLQVLRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYDNDPDESMNSPCQVKQRLQVLRKMLRTSEE 98
 QY 61 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 180
 DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 218
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281
 RESULT 11
 AAY81956
 ID AAY81956 standard; protein; 281 AA.
 XX
 AC AAY81956;
 XX
 DT 10-JUL-2000 (first entry)
 XX
 DE Human Apo-2 ligand protein sequence.
 XX
 KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
 KW therapy; apoptosis; cancer.
 XX
 OS Homo sapiens.
 XX
 PN US6046048-A.
 XX
 PD 04-APR-2000.
 XX
 PF 08-JAN-1997; 97US-00780496.
 XX
 PR 09-JAN-1996; 96US-0009755P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Kim KJ, Ashkenazi AJ, Chuntharapai A;
 XX
 DR WPI; 2000-282690/24.
 DR N-PSDB; AAA07425.
 XX

PT New isolated monoclonal antibodies having antigen specificity for Apo-2
 PT ligand, e.g. 206, 2E11 or 5C2, useful for detecting the expression of Apo
 PT -2 ligand serum, and for treating diseases associated with increased
 PT apoptosis.
 XX
 PS Claim 9; Fig 1a; 46pp; English.
 XX
 CC This sequence is the human Apo-2 ligand protein, which is recognised by
 CC monoclonal antibodies produced by the hybridoma cell lines of the
 CC invention. The hybridoma cell lines are deposited under the American Type
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
 CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
 CC tissues, or serum. The antibodies may also be employed as therapeutics.
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
 CC pathological conditions or diseases associated with increased apoptosis.
 CC They are also useful for the affinity purification of Apo-2 ligand from
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
 CC
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDPDESMNSPCQVKQRLQVLRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYDNDPDESMNSPCQVKQRLQVLRKMLRTSEE 98
 QY 61 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 180
 DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 218
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281
 RESULT 12
 AAB24038
 ID AAB24038 standard; protein; 281 AA.
 XX
 AC AAB24038;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Human PRO1096 protein sequence SEQ ID NO:51.
 XX
 KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumorigenesis; anticancer; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO2000053750-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 02-DEC-1999; 99WO-US028551.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028634.
XX (GETH) GENENTECH INC.
PA Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
PI N-PSDB; AAC58120.
DR WPI; 2000-594320/56.
XX N-PSDB; AAC58120.
XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT the growth of tumors in mammals, and to identify inhibitors of PRO
PT polypeptide activity or expression.
XX Claim 61; Fig 36; 226pp; English.

XX The present invention describes an antibody that binds to a human protein
XX (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
XX PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
XX PRO4407; PRO1555; PRO1036; and PRO2262. (I) has anticancer
XX activity and can be used to diagnose tumors in mammals, by detecting
XX complex formation when the antibody is contacted with test cells.
XX Increased expression of genes encoding (I) can also be detected to
XX diagnose tumors. Agents which inhibit the activity of (I), especially
XX the antibodies, or an antisense oligonucleotide which hybridizes to genes
XX encoding (I), can be used to inhibit tumour growth, preferably by
XX inducing cell death. Methods from the present invention can be used to
XX identify compounds which inhibit the biological activity of (I). AAC58019
XX to AAC58102 represent PCR primers and hybridisation probes used in
XX examples from the present invention for human PRO sequences. AAC58103 to
XX AAC58122 and AAC24021 to AAC24040 represent human PRO polynucleotide and
XX protein sequences given in the exemplification of the present invention

XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGSGIACFLKEDDSYWDNDSESNPCWQVQWQLRQVLRKMLTSEE 60
Db 39 TNELKQMDKYSGSGIACFLKEDDSYWDNDSESNPCWQVQWQLRQVLRKMLTSEE 98
Qy 61 TISTVQEKQNIISPLVREGRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNIISPLVREGRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKDKMQVQYIYKTSYPD 180
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKDKMQVQYIYKTSYPD 218
Qy 181 PILLKMSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281

RESULT 13
AAB08545
ID AAB08545 standard; protein; 281 AA.
XX AC AAB08545;
XX 20-DEC-2000 (first entry)

XX Amino acid sequence of a human TRAIL polypeptide.
XX Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
KW TNF related apoptosis-inducing ligand; tumour cell;
KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
KW non-small cell lung carcinoma.

XX Homo sapiens.
OS WO200048619-A1.
XX 24-AUG-2000.
XX 15-FEB-2000; 2000WO-US003891.
XX 16-FEB-1999; 99US-0120313P.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX Rosen GD;
XX WPI; 2000-558253/51.
XX N-PSDB; AAA64325.
XX Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
PT administration of synergistic combination of diterpenoid diepoxide and
PT tumor necrosis factor related apoptosis-inducing ligand.
XX Disclosure; Page 23-24; 29pp; English.

XX The present sequence represents a human TRAIL (tumour necrosis factor
XX (TNF) related apoptosis-inducing ligand) polypeptide. The specification
XX describes a method for enhanced killing of tumour cells. The method
XX comprises contacting a susceptible tumour cell with a synergistic mixture
XX of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
XX dosage to kill at least 50 % of the cells. This mixture is synergistic,
XX and so is active at lower doses and against otherwise resistant cell
XX lines. The method is used for killing tumour cells, especially solid
XX tumours or carcinomas (especially mammary carcinoma or non-small cell
XX lung carcinoma)

XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGSGIACFLKEDDSYWDNDSESNPCWQVQWQLRQVLRKMLTSEE 60
Db 39 TNELKQMDKYSGSGIACFLKEDDSYWDNDSESNPCWQVQWQLRQVLRKMLTSEE 98
Qy 61 TISTVQEKQNIISPLVREGRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNIISPLVREGRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKDKMQVQYIYKTSYPD 180
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKDKMQVQYIYKTSYPD 218
Qy 181 PILLKMSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281

RESULT 14
AAB28691
ID AAB28691 standard; protein; 281 AA.
XX AC AAB28691;
XX 14-FEB-2001 (first entry)

XX Human AGP-1.
XX Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;

KW	antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW	human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW	hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW	transplant rejection; cardiovascular disease; arteriosclerosis.
XX	
OS	Homo sapiens.
PN	WO2000063253-A1.
XX	
PD	26-OCT-2000.
XX	
PF	24-MAR-2000; 2000WO-US008004.
XX	
PR	16-APR-1999; 99US-00293245.
XX	(AMGE-) AMGEN INC.
XX	
PI	Hsu H, Meng S;
XX	
DR	WPI; 2000-565240/64.
XX	
DR	N-PSDB; AAC67831.
XX	
PT	Fusion protein of AGP-1 protein and an Fc region, used to treat
PT	proliferative disorders, immune disorders, and virally-induced disorders.
XX	
PS	Claim 3; Fig 2; 93pp; English.
XX	
CC	The present sequence is human AGP-1, a type II transmembrane protein.
CC	Fusion proteins comprising an Fc immunoglobulin region fused to the N-
CC	terminal portion of the AGP-1 protein have been produced. The fusion
CC	proteins can be used to induce apoptosis in a tissue, and to treat
CC	proliferative disorders, immune disorders, or virally-induced disorders.
CC	The proliferative disorders include cancers, such as breast, prostate,
CC	lung or colon cancer. The viral infections include hepatitis, and
CC	acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC	be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC	such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC	proteins have increased biological activity compared to the soluble AGP-1
XX	proteins used in prior art therapies
XX	
SO	Sequence 281 AA;

Query Match	100.0%	Score 1287;	DB 3;	Length 281;
Best Local Similarity	100.0%;	Prod. No. 2.3e-117;		
Matches 243;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TNELKQMDKYSKSGIACFLKXEDDSYNDPDEESMNSPCWQVKQLRQLRVKMLIRTSEE	60	
Db	39	TNELKQMDKYSKSGIACFLKXEDDSYNDPDEESMNSPCWQVKQLRQLRVKMLIRTSEE	98	
Qy	61	TISTVQEKQOINISPLVBERGQORVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSR	120	
Db	99	TISTVQEKQOINISPLVBERGQORVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSR	158	
Qy	121	SGHSFLSNLHNRGELVTHEKGFYYIYSQTYFRFQEEIKENTKDKQWQVIYKYTSPD	180	
Db	159	SGHSFLSNLHNRGELVTHEKGFYYIYSQTYFRFQEEIKENTKDKQWQVIYKYTSPD	218	
Qy	181	PILLMKSARNCSWKDABYGYISYOGGIPELKENDRIFVSVTTHEILDMDHASFFGAF	240	
Db	219	PILLMKSARNCSWKDABYGYISYOGGIFELKENDRIFVSVTTHEILDMDHASFFGAF	278	
Qy	241	LVG 243		
Db	279	LVG 281		

RESULT 15
AAB50977
ID AAB50977 standard; protein; 281 AA.
XX
AC AAB50977;
XX

DT	21-MAR-2001	(first entry)
XX		
DE	Human PRO1096 protein.	
XX		
KW	Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;	
KX	antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;	
KW	PRO agonist; cancer; inflammatory disorder; immunological disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200073348-A2.	
XX		
PD	07-DEC-2000.	
XX		
PP	30-MAY-2000; 2000WO-US014941.	
XX		
PR	02-JUN-1999; 99WO-US012252.	
22-JUN-1999;	99US-0140650P.	
PR	23-JUN-1999; 99US-0141037P.	
PR	20-JUL-1999; 99US-0144758P.	
PR	01-SEP-1999; 99WO-US020111.	
PR	08-SEP-1999; 99WO-US020594.	
PR	29-OCT-1999; 99US-0162506P.	
PR	30-NOV-1999; 99WO-US028313.	
PR	01-DEC-1999; 99WO-US028634.	
PR	02-DEC-1999; 99WO-US028551.	
PR	09-DEC-1999; 99US-0170262P.	
PR	16-DEC-1999; 99WO-US030095.	
PR	20-DEC-1999; 99WO-US030999.	
PR	06-JAN-2000; 2000WO-US000376.	
PR	11-FEB-2000; 2000WO-US003565.	
PR	18-FEB-2000; 2000WO-US004341.	
PR	18-FEB-2000; 2000WO-US004342.	
PR	03-MAR-2000; 2000WO-US005841.	
PR	10-MAR-2000; 2000US-0187202P.	
PR	15-MAR-2000; 2000WO-US006319.	
PR	30-MAR-2000; 2000WO-US006884.	
PR	17-MAY-2000; 2000WO-US008439.	
XX		
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;	
PI	Shelton DL, Smith V, Watanabe CK, Wood WI;	
XX		
DR	WPI; 2001-016509/02.	
DR	N-PSDB; AAC91579.	
XX		
PT	Twenty eight nucleic acids encoding PRO polypeptides which are useful for	
PT	treating various tumors, e.g. breast cancer, and other inflammatory,	
XX	angiogenic and immunological disorders.	
XX		
PS	Claim 31; Fig 54; 188pp; English.	
XX		
CC	The present sequence is one of twenty eight novel PRO polypeptides. The	
CC	PRO polypeptides and their agonists, including antibodies, peptides, and	
CC	small molecule agonists, may be used to treat various tumours, e.g.,	
CC	cancers such as breast cancer, ovarian cancer, renal cancer, colorectal	
CC	cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,	
CC	central nervous system cancer, melanoma or leukaemia. They are also	
CC	useful for treating other disorders such as neuronal, glial, astrocytal,	
CC	hypothalamic and other glandular, macrophagal, epithelial, stromal and	
CC	biastocoealic disorders, and inflammatory, angiogenic and immunological	
XX	disorders	
SO	Sequence 281 AA:	

```

Query Match      100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 TNELKQMDKYKSGIAFLKEDPSYMDPNDESNSPCWQVQWQLRGLRVKMLRTSEE 60

```


Db 39 TNELQWQDKYKSGIACFLKEDDSYWDNDDEESMNSPCWQVQWQLRVKWLRTSEE 98
 QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 180
 Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 218
 QY 181 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
 Db 219 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

RESULT 16

AAB67243
 ID AAB67243 standard; protein; 281 AA.

AC AAB67243;

DT 18-APR-2001 (first entry)

DE Human Apo2 ligand.

XX Human; Apo2 ligand: divalent metal ions; viral infection; cancer.

OS Homo sapiens.

PN WO200100832-A1.

XX 04-JAN-2001.

PF 26-JUN-2000; 2000WO-US017579.

PR 28-JUN-1999; 99US-0141342P.

XX (GETH) GENENTECH INC.

PA Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;

PI O'connell M, Pai R, Shahrokh Z, Simmons L;

DR WPI; 2001-123012/13.

XX Use of divalent metal ions for making Apo-2 ligand and in formulations
 PT containing Apo-2 ligand for increasing yield and stability of ligand
 PT trimers, useful for therapeutic applications.

XX Claim 6; Fig 1; 60pp; English.

PS The present invention relates to a formulation comprising Apo-2 ligand
 CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
 CC treating cancers and viral infections. Addition of divalent metal ions
 CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
 CC in increased yield and stability of Apo-2 ligand trimers

XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELQWQDKYKSGIACFLKEDDSYWDNDDEESMNSPCWQVQWQLRVKWLRTSEE 60

Db 39 TNELQWQDKYKSGIACFLKEDDSYWDNDDEESMNSPCWQVQWQLRVKWLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 180
 Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 218
 QY 181 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
 Db 219 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

RESULT 17

AAE11031

ID AAE11031 standard; protein; 281 AA.

XX AAE11031;

DT 18-DEC-2001 (first entry)

DE Human TNF related apoptosis inducing ligand (TRAIL) protein.

XX Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
 KW melanoma.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Domain 1..18

FT Region 19..38

FT Domain 39..281

FT Domain 39..281

FT Domain 39..281

FT Domain 39..281

PN US6284236-B1.

XX 04-SEP-2001.

XX 26-MAY-1999; 99US-00320424.

XX 29-JUN-1995; 95US-00496632.

XX 01-NOV-1995; 95US-00548368.

XX 25-JUN-1996; 96US-00670354.

XX 26-MAR-1998; 98US-00048641.

XX 10-NOV-1998; 98US-00190046.

XX (IMMV) IMMUNEX CORP.

XX Wiley SR, Goodwin RG;

XX WPI; 2001-595463/67.

DR N-ESDB; AAD18395.

XX New tumor necrosis factor related apoptosis inducing ligand polypeptides
 PT for treating viral infections (e.g. bovine viral diarrhoea or human
 PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).

XX Claim 2; Col 45-48; 41pp; English.

PS The invention relates to a cytokine designated as tumour necrosis factor
 CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
 CC of certain target cells, including cancer cells and virally infected
 CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
 CC treating viral infections (e.g. bovine viral diarrhoea or human
 CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
 CC melanoma), as a research reagent useful in studying apoptosis including
 CC the regulation of programmed cell death. TRAIL DNA sequences may be
 CC employed in developing a gene therapy approach to treating disorders

CC mediated by defective or insufficient amounts of TRAIL, in the production
CC of TRAIL polypeptides and as probes or primers in polymerase chain
CC reactions (PCR). The present sequence is human TRAIL protein
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDP 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDP 218
QY 181 PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281
RESULT 18
AAB48350
ID AAB48350 standard; protein; 281 AA.
XX
AC AAB48350;
XX
DT 20-APR-2001 (first entry)
XX
DE Human TL2 polypeptide.
XX
XX Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
KW anti-inflammatory; immunosuppressive; cerebroprotective; vasotropic;
KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;
KW neutropic; neuroprotective; antiarthritic; antirheumatic; antischismic;
KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200077191-A1.
XX
PD 21-DEC-2000.
XX
PF 12-JUN-2000; 2000WO-US016134.
XX
PR 15-JUN-1999; 98US-00333593.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
XX
DR WPI; 2001-112223/12.
DR N-PSDB; AAC84745.
XX
XX New tumor necrosis factor related receptor TR6 polynucleotides and
PT polypeptides useful for e.g. for treating chronic and acute inflammation,
PT arthritis, septicemia, autoimmune diseases, infection, cancer, bone
PT diseases.
XX
PS Disclosure; Page 26; 47pp; English.
XX
CC The invention relates to a human tumour necrosis factor (TNF) related
CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.

CC The TR6 polypeptides are useful for treating chronic and acute
CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
CC host disease, infection, stroke, ischaemia, acute respiratory disease
CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
CC atherosclerosis, and Alzheimer's disease. These may also be used to
CC inhibit production of TNF-alpha and eicosanoids, as research reagents and
CC materials for discovering treatments and diagnostics to animal and human
CC diseases. The polypeptides may further be used as immunogens to produce
CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides
CC may also be used as hybridization probes for cDNA and genomic DNA, for
CC isolating full-length cDNAs and genomic clones encoding TR6 and of other
CC genes having high sequence similarity to TR6 gene, and for chromosome
CC identification. The present sequence represents a human TL2 polypeptide.
CC TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is
CC a ligand for the TL2 polypeptide
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDP 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDP 218
QY 181 PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281
RESULT 19
ABB08133
ID ABB08133 standard; protein; 281 AA.
XX
AC ABB08133;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human TRAIL polypeptide.
XX
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
KW tuberculostatic; cytostatic; human; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200236141-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US044834.
XX
PR 02-NOV-2000; 2000US-0245721P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
PI Thomas EK;
XX

DR WPI; 2002-500114/53.
 XX Treating an individual suffering from infection, e.g. inflammation,
 PT chickenpox or AIDS, by administering a combination of dendritic cell
 PT mobilization factor or maturation agent, T cell enhancing factor and
 PT antigen-specific T cells.
 XX
 XX
 PS Disclosure; Page 40-42; 43pp; English.
 XX
 CC The invention relates to treating an individual at risk for or suffering
 CC from infection with a pathogenic or opportunistic organism. The method
 CC involves administering a combination of two to five agents comprising:
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
 CC or (e) activated, antigen-specific T cells. The methods are useful for
 CC treating an individual at risk for or suffering from infection with a
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
 CC T. cruzi, which causes Chaga's disease). The methods are especially
 CC useful for treating an individual suffering from immunosuppression by
 CC enhancing a lymphocyte-mediated immune response. In particular, the
 CC method is useful for treating inflammations, chickenpox, oral or genital
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
 CC cell leukemia or T cell lymphoma. The activated antigen-presenting
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence
 CC represents a human TRAIL polypeptide fragment
 XX
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELQMDKYSKSGIACFLKEDSYNDPNDDEESMNSPCWQVKQLRQVRLTSEE 60
 DB 39 TNELQMDKYSKSGIACFLKEDSYNDPNDDEESMNSPCWQVKQLRQVRLTSEE 98
 QY 61 TISTVQEQKQNTISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEQKQNTISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSLNHLNRLNGELVTHEKGFYIYSQTYFRFOEIKENTQDKQVQIYKYTSYD 180
 DB 159 SGHSLNHLNRLNGELVTHEKGFYIYSQTYFRFOEIKENTQDKQVQIYKYTSYD 218
 QY 181 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

RESULT 20
 ABG31630
 ID ABG31630 standard; protein; 281 AA.
 XX
 XX ABG31630;
 XX
 XX 29-NOV-2002 (first entry)
 XX
 XX Human TRAIL protein.
 DE
 XX Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
 XX dendritic cell maturation agent; T cell enhancing factor; skin cancer;
 XX antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
 XX brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
 XX actinic keratosis; dendritic cell maturation stimulator; cytostatic;
 XX dendritic cell activator; T cell enhancer; human; TRAIL.
 OS Homo sapiens.
 XX

PN WO200266044-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 23-OCT-2001; 2001WO-US046254.
 XX
 PR 24-OCT-2000; 2000US-0242868P.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;
 PI WPI; 2002-674891/72.
 XX
 XX Treating an individual with tumors or cancers, e.g. liver cancer or brain
 PT tumor, by administering a combination of dendritic cell populations, T
 PT cell enhancing factors and activated, antigen-specific T cells.
 XX
 PS Disclosure; Page 41-43; 44pp; English.
 XX
 CC The present invention relates to a new method for treating a tumour-
 CC bearing subject. The method involves administering a combination of 2 to
 CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell
 CC maturation agent, tumour-killing agent, T cell enhancing factor or
 CC activated, antigen-specific T cells. The method is useful for treating
 CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
 CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
 CC cervical intraepithelial neoplasia. The present amino acid sequence
 CC represents the human TRAIL protein that was used in the method of the
 CC invention
 XX
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELQMDKYSKSGIACFLKEDSYNDPNDDEESMNSPCWQVKQLRQVRLTSEE 60
 DB 39 TNELQMDKYSKSGIACFLKEDSYNDPNDDEESMNSPCWQVKQLRQVRLTSEE 98
 QY 61 TISTVQEQKQNTISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEQKQNTISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSLNHLNRLNGELVTHEKGFYIYSQTYFRFOEIKENTQDKQVQIYKYTSYD 180
 DB 159 SGHSLNHLNRLNGELVTHEKGFYIYSQTYFRFOEIKENTQDKQVQIYKYTSYD 218
 QY 181 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

RESULT 21
 AAU75062
 ID AAU75062 standard; protein; 281 AA.
 XX
 XX AAU75062;
 XX
 XX 23-APR-2002 (first entry)
 XX
 XX Human TNF related apoptosis inducing ligand (TRAIL) protein.
 DE
 XX TRAIL; TNF; apoptosis; tumour; death domain receptor ligand;
 XX diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma;
 XX mammary adenocarcinoma; non-small cell lung carcinoma;
 XX neurological malignancy; haematological malignancy; lichen planus;
 XX non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
 XX

KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
 KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
 KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
 KW discoid lupus erythematosus; human.
 XX Homo sapiens.
 XX US6329148-B1.
 XX 11-DEC-2001.
 XX 15-FEB-2000; 2000US-00505250.
 XX 16-FEB-1999; 99US-0120313P.
 XX 20-AUG-1999; 99US-0149989P.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX Rosen GD, Kao P;
 XX WPI; 2002-121125/16.
 XX N-PSDB; ABK13132.
 XX Use of a synergistic combination of death domain receptor ligands and
 PT diterpenoid triepoxides for killing of tumor cells.
 XX Disclosure; Col 17-20; 20pp; English.
 XX This invention relates to a novel method for enhanced killing of tumor
 CC cells comprising contacting a tumor cell with a synergistic combination
 CC of a death domain receptor ligand and a diterpenoid triepoxide. This
 CC method has cytostatic activity and works by blocking TNF-alpha mediated
 CC induction of c-IAP2 and c-IAP1. The method of the invention may be used
 CC for treating tumors, particularly solid tumors, e.g. carcinoma, mammary
 CC adenocarcinoma and non-small cell lung carcinoma also neurological
 CC malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma,
 CC chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis
 CC fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-
 CC cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid
 CC lupus erythematosus, lichen planus. The combination may be administered
 CC with other active agents, e.g. anti-metastatic, anti-tumour or anti-
 CC angiogenic agents. The potent synergy between the diterpenoids and the
 CC death domain ligands allows increased killing at equivalent or lower
 CC doses, and can sensitize otherwise resistant cells. This sequence
 CC represents the human TNF related apoptosis inducing ligand (TRAIL)
 CC protein sequence. TRAIL is a death domain receptor used in the used
 CC method of the invention in combination with diterpenoid triepoxides to
 CC kill tumors by induction of apoptosis
 XX
 XX Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPDESNMSPCQVQWQLRQLVRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPDESNMSPCQVQWQLRQLVRKMLRTSEE 98
 QY 61 TISTVQEKQNIISPLVREERGFQVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNIISPLVREERGFQVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLNLHRLNGELVHKGFIYISQYFPEFQBEIKENTKNDKQVYIKYTSYDP 180
 DB 159 SGHSFLNLHRLNGELVHKGFIYISQYFPEFQBEIKENTKNDKQVYIKYTSYDP 218
 QY 181 PILLMKARSNCWSKDAEYGLISTYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKARSNCWSKDAEYGLISTYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 |||

Db 279 LVG 281
 RESULT 22
 AAMS1077
 ID AAMS1077 standard; protein; 281 AA.
 XX AAMS1077;
 AC AAMS1077;
 DT 30-MAY-2002 (first entry)
 XX Human Apo-2 ligand (TRAIL).
 DE Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour;
 KW antitumour; therapy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Protein 114..281
 FT /note= "Apo-2L polypeptide used in method of Claim 18"
 XX WO200209755-A2.
 PN 07-FEB-2002.
 XX 27-JUL-2001; 2001WO-US023691.
 XX 27-JUL-2000; 2000US-0221256P.
 XX (GETH) GENENTECH INC.
 PI Escandon E, Fox JA, Kelley SK, Xiang H;
 XX WPI; 2002-268997/31.
 XX Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I
 PT inhibitor class, and Apo-2 ligand receptor agonist for enhancing
 PT apoptosis in mammalian cells, or for treating cancer in a mammal.
 XX Claim 18; Page 79-80; 84pp; English.
 XX The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The
 CC invention relates to methods of inducing apoptosis in mammalian cells,
 CC and especially to the use of Apo-2L receptor agonists and CPT-11 (a
 CC chemotherapeutic agent of the topoisomerase I inhibitor class) to
 CC synergistically induce apoptosis in mammalian cells, in particular
 CC mammalian cancer cells, and especially colorectal cancer cells (Claimed).
 CC The cells may be in cell culture or in a mammal, e.g. a mammal suffering
 CC from cancer or a condition in which induction of apoptosis in the cells
 CC is desirable. A claimed method of treating cancer in a mammal comprises
 CC administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is
 CC administered about 6-72 hours prior to administration of the Apo-2L
 CC receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L
 CC (especially amino acids 114-281 of the present sequence) and anti-DR4 or
 CC anti-DR5 receptor antibodies. Exposure of the cancer cells to CPT-11 and
 CC Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors,
 CC directing the cells towards an apoptotic pathway rather than cell cycle
 CC arrest and possible DNA repair, thus providing enhanced antitumour
 CC activity. An example illustrates the synergistic inhibition of tumour
 CC growth by Apo-2L and CPT-11 in athymic nude mice injected s.c. with human
 CC COLO205 colon carcinoma cells
 XX
 XX Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPDESNMSPCQVQWQLRQLVRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPDESNMSPCQVQWQLRQLVRKMLRTSEE 98

Qy	61	TISTVQEKQOINTSPLVRRGEPQORAAHITGTRGRSNTLSPNSGKNEKALGRKINSWESSR	120
Db	99	TISTVQEKQOINTSPLVRRGEPQORAAHITGTRGRSNTLSPNSGKNEKALGRKINSWESSR	158
Qy	121	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRQEIEIKENTKNDKQMWQYIYKYTSYFD	180
Db	159	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRQEIEIKENTKNDKQMWQYIYKYTSYFD	218
Qy	181	PILLMKRSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240
Db	219	PILLMKRSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278
Qy	241	LVG 243	
Db	279	LVG 281	
RESULT 23			
ABP51954			
ID	ABP51954 standard; protein; 281 AA.		
XX	AC ABP51954;		
XX	09-OCT-2002 (first entry)		
DE	Human Apo-2 ligand protein sequence SEQ ID NO:4.		
XX	Bacterial host; protease; degP; prc; spr; anti-VEGF antibody; antibody;		
KW	humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;		
KW	anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;		
KW	anti-CD11a; Fab'; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.		
XX	Homo sapiens.		
XX	WO200248376-A2.		
PN	20-JUN-2002.		
PD	07-DEC-2001; 2001WO-US047581.		
XX	14-DEC-2000; 2000US-0256162P.		
PR	(GETH) GENENTECH INC.		
XX	Chen CY;		
XX	WPI; 2002-583522/62.		
XX	N-PSDB; ABQ73920.		
XX	Novel Escherichia coli strain useful for producing polypeptide, deficient		
PT	in degp and prc encoding protease, and harboring mutant spr gene, product		
PT	of gene suppresses growth phenotypes of strains harboring prc mutants.		
XX	Example 1; Fig 4; 63pp; English.		
PS			

CC	fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
CC	tissue factor Fab/2-leucine zipper fusion with a 6-histidine tag, or anti
CC	-CD18 Fab/2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
CC	Fab/2-leucine zipper fusion with a 6-lysine tag. The present sequence
CC	represents a human Apo-2 ligand amino acid sequence from the present
CC	invention
XX	
SQ	Sequence 281 AA;
	Query Match 100.0%; Score 1287; DB 5; Length 281;
	Best Local Similarity 100.0%; Pred. No. 2.3e-117;
	Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 TNELKQMDKYSGSIACFLKEDDSYDNPDESMNSPCWQVKWLQLVKKMLRTSEE 60
Dd	39 TNELKQMDKYSGSIACFLKEDDSYDNPDESMNSPCWQVKWLQLVKKMLRTSEE 98
Qy	61 TISTVQEKQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEXALGRKINSWESSR 120
Dd	99 TISTVQEKQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEXALGRKINSWESSR 158
Qy	121 SGHSFSLNHLRNGLVIHEKGFIYYSQTYYFRQPBEIKENTKNDKOMVOIYKYTSYPD 180
Dd	159 SGHSFSLNHLRNGLVIHEKGFIYYSQTYYFRQPBEIKENTKNDKOMVOIYKYTSYPD 218
Qy	181 PILMKARNSCSWKDAEYGLYSTYOGGIPELKENDRI FVSVTNEHLIDMDHEASFFGAF 240
Dd	219 PILMKARNSCSWKDAEYGLYSTYOGGIPELKENDRI FVSVTNEHLIDMDHEASFFGAF 278
Qy	241 LVG 243
Dd	279 LVG 281
RESULT 24	
AAO19095	
ID	AAO19095 standard; protein; 281 AA.
XX	
AC	AAO19095;
XX	
DT	22-NOV-2002 (first entry)
XX	
DE	C neoforms antigen expressing dendritic cell related protein #4.
XX	
KW	Human; fungicide; fungal infection; dendritic cell; antigen;
XX	Cryptococcus neoformans; vaccine; immunostimulant.
OS	Homo sapiens.
XX	
FN	WO200266053-A2.
XX	
PD	29-AUG-2002.
XX	
PF	14-DEC-2001; 2001WO-US048288.
XX	
PR	04-JAN-2001; 2001US-0259653P.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Thomas EK;
XX	
DR	WPI; 2002-674896/72.
XX	
PT	Producing a population of activated, Cryptococcus neoformans antigen-
PT	presenting dendritic cells for preventing or treating C. neoformans
PT	infection comprises causing the obtained dendritic cells to present the
PT	antigen.
XX	
PS	Disclosure; Page 29-30; 32pp; English.
XX	
CC	The present invention relates to a method of producing a population of
CC	activated, Cryptococcus neoformans antigen-presenting dendritic cells,
CC	comprising causing the obtained dendritic cells to present the antigen

CC and maturing the dendritic cells. The activated, C. neoformans antigen-
CC expressing dendritic cells are useful for treating, or as vaccines or
CC vaccine adjuvants against, C. neoformans infection, or for generating
CC antigen-specific T cells. The present sequence is a human protein shown
CC in the exemplification of the invention
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDPNDESMSNSPCWQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESMSNSPCWQVKWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQNI8PLVRERGQORVAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNI8PLVRERGQORVAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIKYTSYPD 180
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIKYTSYPD 218
QY 181 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 25
AAU79593
ID AAU79593 standard; protein; 281 AA.
XX
AC AAU79593;
XX
DT 24-SEP-2002 (first entry)
XX

XX Human TNF-related apoptosis inducing ligand (TRAIL) protein.
DE Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
XX tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26.
XX

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 1..16
FT Domain /note= "Cytoplasmic domain"
FT Domain 17..38
FT Domain /note= "Transmembrane domain"
FT Domain 39..281
FT Domain /note= "Extracellular domain"
FT Domain 118..256
FT Domain /note= "TNF domain"

XX US2002061525-A1.
XX
XX 23-MAY-2002.
XX
XX 16-MAY-2001; 2001US-00855544.
XX
XX 16-MAY-2000; 2000IL-00136156.
XX
XX (YELI/) YELIN R.
XX (KHOS/) KHOSRAVI R.
PA

PA (SAVI/) SAVITZKY K.
XX
XX Yelin R, Khosravi R, Savitzky K;
XX
XX WPI; 2002-479259/51.
DR

XX New splice variants of tumor necrosis factor-related apoptosis inducing
PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
PT diseases or disorders associated with low expression of the variants.
XX
XX Disclosure; Fig 9; 29pp; English.
PS
XX

XX The invention discloses isolated, naturally occurring, polypeptide splice
CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing
CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal
CC cellular differentiation and development of multicellular organisms.
CC Apoptosis is induced by certain cytokines which include TNF and TRAIL
CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane
CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in
CC many tissues and cells. Receptors for TRAIL include two death domain
CC containing receptors, DR4 and DR5, as well as two decoy receptors, DCR1
CC and DCR2, lacking the intracellular signalling death domain. TRAIL,
CC induced by type I interferons, induces apoptosis in tumour cells, whereas
CC normal cells are relatively resistant without showing significant toxic
CC side effects. Thus, TRAIL has the potential to be a very useful
CC antitumour agent. The naturally occurring splice variants may differ in
CC their cellular distribution, expression levels/timing and activity.
CC Determining these factors could provide possible mechanisms for the
CC induction of apoptosis of tumours cells. The splice variant polypeptides
CC and polynucleotides can be used in gene therapy, to raise antibodies, to
CC detect the levels, distribution and ratios of expression of TRAIL, and
CC its splice variants, in a biological sample and to identify compounds
CC which bind the variant TRAIL products and modulate its activity (agonists
CC and antagonists). Pharmaceutical compositions, comprising an expression
CC vector or any of the amino acid sequences, are useful for causing a
CC cytotoxic effect in cancer cells and for treatment of diseases which can
CC be ameliorated, cured or prevented by lowering or raising the level of
CC the amino acid sequences. The antibodies may also have a therapeutic
CC utility in blocking or decreasing the activity of the TRAIL variant
CC products. Diseases that may be treated include cancer, neurodegenerative
CC diseases, autoimmune diseases, diseases involved in the non-normal
CC development of tissues and aging. TRAIL's gene is located on chromosome
CC 3q26. The sequence presented is the wild-type human TNF-related apoptosis
CC inducing ligand (TRAIL) protein
XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDPNDESMSNSPCWQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESMSNSPCWQVKWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQNI8PLVRERGQORVAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNI8PLVRERGQORVAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIKYTSYPD 180
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIKYTSYPD 218
QY 181 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 26

ABG73861
ID ABG73861 standard; protein; 281 AA.
XX AC ABG73861;
XX DT 03-APR-2003 (first entry)
XX DE Human Apo-2 ligand protein.
XX Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;
XX nuclear factor-kappa B; NF-kappa B; Apo-2 ligand; AIDS;
XX tumour necrosis factor receptor; acquired immunodeficiency syndrome;
XX Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;
XX aplastic anaemia; myocardial infarction; stroke; reperfusion injury;
XX toxin-induced liver disease; cancer; lupus; herpes virus infection.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Domain 15..40
FT /note= "Transmembrane domain"
FT Domain 41..281
FT /note= "Extracellular domain"
FT Modified-site 109
FT /note= "N-glycosylated"
XX US6462176-B1.
XX 08-OCT-2002.
XX 11-SEP-1997; 97US-00928069.
XX 23-SEP-1996; 96US-0026943P.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ;
XX WPI; 2003-173840/17.
XX N-PSDB; ABX15469.
XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
XX mammalian cells, for generating antibodies, in affinity purification
XX techniques, and in competitive-type receptor binding assays.
XX Example 4; Fig 4; 52pp; English.
XX The invention relates to an Apo-3 polypeptide having an extracellular
XX domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
XX has been found to stimulate or induce apoptotic activity in mammalian
XX cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
XX receptor (TNFR) family of polypeptides. The invention also relates to a
XX chimeric molecule comprising an extracellular domain sequence comprising
XX residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
XX Apo-3 polypeptide is useful therapeutically to induce apoptosis in
XX mammalian cells. Decreased levels of apoptosis has been associated with
XX conditions such as cancer, lupus, and herpes virus infection. Increased
XX levels of apoptosis are associated with diseases such as acquired
XX immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
XX disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
XX pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
XX infarction, stroke, reperfusion injury, and toxin-induced liver disease.
XX The Apo-3 polypeptide is also useful in non-therapeutic applications such
XX as in quantitative diagnostic assays as a control against which samples
XX containing unknown quantities of Apo-3 may be prepared, in generating
XX antibodies, as standards in assays for Apo-3, in affinity purification
XX techniques, and in competitive-type receptor binding assays. The chimeric
XX molecule is useful therapeutically to inhibit apoptosis or nuclear factor
XX -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
XX Apo-3 antibodies. The present sequence represents polypeptide sequence of
XX the human Apo-2 ligand protein which is also reported to be involved in
XX apoptotic cell death. In the current invention the apoptotic activity of

CC the Apo-2 ligand protein was measured on human lymphoid cells
XX Sequence 281 AA;
Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. NO. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWLQRLVRKMILRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWLQRLVRKMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAHAITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAHAITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKDKQMVQYIYKITSYPD 180
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKDKQMVQYIYKITSYPD 218
QY 181 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAP 240
DB 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAP 278
QY 241 LVG 243
DB 279 LVG 281
RESULT 27
ABU10205
ID ABU10205 standard; protein; 281 AA.
XX AC ABU10205;
XX DT 11-AUG-2003 (first entry)
XX DE Human Apo-2 ligand.
XX Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; cancer;
XX neurodegenerative disease; immunosuppressive; tissue typing.
XX OS Homo sapiens.
XX PN US2003004313-A1.
XX 02-JAN-2003.
XX 28-MAR-2002; 2002US-00112193.
XX 23-SEP-1996; 96US-0026943P.
XX 11-SEP-1997; 97US-00928069.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ;
XX WPI; 2003-438872/41.
XX N-PSDB; ACA61696.
XX New isolated Apo-3 polypeptides, useful for stimulating or inducing
XX apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
XX or ex vivo gene therapy techniques.
XX Example 4; Fig 4; 50pp; English.
XX The invention relates to an isolated Apo-3 polypeptide. The Apo-3
XX polypeptides are useful for stimulating or inducing apoptotic activity in
XX mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
XX techniques. The Apo-3 chimeric molecules are useful for inhibiting
XX apoptosis, or as immunogens used in generating antibodies. The
XX antagonistic antibodies may be used to block excessive apoptosis, for
XX instance in neurodegenerative disease, or to block potential autoimmune/

CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The
 CC nucleic acid sequences are useful as diagnostics for tissue-specific
 CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
 CC knockout animals. The transgenic or knockout animals are useful in
 CC developing and screening of therapeutically useful reagents. The present
 CC sequence represents the amino acid sequence of human Apo-2 ligand
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGTACFLKDDSYWDPNDESNPCQVQWQLROLVRCMLRTSEE 60
 DB 39 TNELKQMDKYSKSGTACFLKDDSYWDPNDESNPCQVQWQLROLVRCMLRTSEE 98
 QY 61 TISTVQEKQNTISPLVRERGPQVAHITGRGNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNTISPLVRERGPQVAHITGRGNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHRLNGELVIEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPD 180
 DB 159 SGHSFLSNLHRLNGELVIEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPD 218
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGIFELKENDRIEVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGIFELKENDRIEVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281
 RESULT 28
 ABU71443
 ID ABU71443 standard; protein; 281 AA.
 XX
 AC ABU71443;
 DT 09-JUN-2003 (first entry)
 DE Human neoplasia inhibiting PRO polypeptide PRO1096.
 DE
 XX Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;
 KW ovarian cancer; renal cancer; colorectal cancer; melanoma;
 KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
 KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
 KW central nervous system cancer; hepatic carcinoma; glioblastoma;
 KW neuronal disorder; glial disorder; astrocytal disorder;
 KW hypothalamic disorder; glandular disorder; macropagal disorder;
 KW epithelial disorder; stromal disorder; blastocoelec disorder;
 KW inflammatory disorder; angiogenic disorder; immunologic disorder.
 XX
 OS Homo sapiens.
 XX
 XX US2002192209-A1.
 XX
 PD 19-DEC-2002.
 XX
 XX 30-NOV-2001; 2001US-00001054.
 XX
 PR 17-SEP-1997; 97US-0059114P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 30-MAR-1998; 98US-0079320P.
 PR 24-APR-1998; 98US-0082999P.
 PR 29-APR-1998; 98US-0083545P.
 PR 12-MAY-1998; 98US-0085149P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 25-JUN-1998; 98US-0090691P.
 PR 17-AUG-1998; 98US-0096891P.
 PR 17-AUG-1998; 98US-0096894P.

PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98US-0100263P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 18-NOV-1998; 98US-0108049P.
 PR 19-NOV-1998; 98US-00180997.
 PR 15-DEC-1998; 98US-0112420P.
 PR 22-DEC-1998; 98US-00218517.
 PR 22-DEC-1998; 98US-0113296P.
 PR 05-JAN-1999; 99WO-US0000106.
 PR 12-JAN-1999; 99US-0115554P.
 PR 12-JAN-1999; 99US-0115558P.
 PR 20-JAN-1999; 99US-0116333P.
 PR 08-MAR-1999; 99WO-US0005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-APR-1999; 99US-00284291.
 PR 20-APR-1999; 99WO-US0008615.
 PR 27-APR-1999; 99US-0131294P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 22-JUN-1999; 99US-0140650P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 25-AUG-1999; 99US-00380137.
 PR 01-SEP-1999; 99US-00380138.
 PR 08-SEP-1999; 99WO-US020594.
 PR 09-SEP-1999; 99US-00380913.
 PR 18-OCT-1999; 99US-00403297.
 PR 29-OCT-1999; 99US-0162506P.
 PR 10-NOV-1999; 99US-00423741.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 25-MAY-2001; 2001US-00866034.
 PR 01-JUN-2001; 2001US-00872034.
 PR 01-JUN-2001; 2001US-00872035.
 PR 14-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00927796.
 PR 09-AUG-2001; 2001US-00929404.
 PR 28-AUG-2001; 2001US-00941392.
 PR 29-AUG-2001; 2001WO-US027099.

PR 04-SEP-2001; 2001US-00946374.
PA (GETH) GENENTECH INC.
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC,
PI Shelton DU, Smith V, Watanabe CK, Wood WI;
XX WPI; 2003-328851/06.
DR N-PSDB; ACAS8016.
XX
XX Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT treating tumor, preferably cancer, or for treating neuronal, glial,
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders.
XX
XX Claim 32; Fig 54; 186pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
CC associated signal peptide or PRO polypeptide extracellular domain with or
CC without its associated signal peptide. The PRO polypeptide or an antibody
CC binding to it is useful for inhibiting the growth of a tumor cell. A
CC composition containing a PRO polypeptide is useful for inhibiting
CC neoplastic cell growth or for treating a tumour, preferably cancer (such
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system
CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
CC agonists. The PRO polypeptide or an antibody binding to it is useful in
CC the preparation of a medicament for treating a condition which is
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO
CC polypeptide or an antibody binding to it is also useful for treating
CC neuronal glial, astrocytal, hypothalamic, glandular, macrophagal,
CC epithelial, stromal, blastocoealic, inflammatory, angiogenic and
CC immunologic disorders. The present sequence represents the amino acid
XX sequence of a PRO polypeptide of the invention
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;

QY 1 TNELQMDDKYSKSGIACFLKEDDSYDNDDEESMNSPCWQVQLRQLVRLKMLRTSEE 60
Db 39 TNELQMDDKYSKSGIACFLKEDDSYDNDDEESMNSPCWQVQLRQLVRLKMLRTSEE 98

QY 51 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYD 180
Db 159 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYD 218

QY 241 LVG 243
Db 279 LVG 281

RESULT 29
ABG72738
ID ABG72738 standard; protein; 281 AA.
XX
XX ABG72738;
XX
XX
DT 17-FEB-2003 (first entry)
XX
DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.

XX
KW Human; allergic disease; allergy; TNF; TRAIL; diagnosis;
KW tumour necrosis factor-related apoptosis inducing ligand;
KW atopic skin inflammation.
XX
OS Homo sapiens.
XX
XX WO200283946-A1.
XX
XX 24-OCT-2002.
XX
XX 01-MAR-2002; 2002WO-JP001914.
XX
XX 06-APR-2001; 2001JP-00108631.
XX
XX (GENO-) GENOX RES INC.
XX (NICE-) JAPAN GEN AGENCY NATION.
XX
XX Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
XX WPI; 2003-093037/08.
XX N-PSDB; ABX13715.
XX
XX Measurement of the expression level of TNF related apoptosis inducing
PT ligand gene for diagnosis and examination of allergic disease and
PT screening agents for allergic disease treatment.
XX
XX Disclosure; Page 51-52; 58pp; Japanese.
XX
XX The invention discloses a method for examining allergic diseases, which
CC comprises measuring the expression level of tumour necrosis factor (TNF)-
CC related apoptosis inducing ligand (TRAIL) gene in a specimen from the
CC patient and comparing this level with the level in healthy persons. TRAIL
CC gene expression is decreased in patients. The nucleic acids and
CC polypeptide can be used to screen for agents for the treatment of
CC allergic diseases, possibly using a transgenic rodent as a model animal
CC for the disease, with effectiveness determined by changes in expression
CC levels or protein activity. The method is useful for the diagnosis,
CC examination, prevention and treatment of allergic diseases, including
CC atopic skin inflammation. The sequence presented is the human TRAIL
CC protein
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;

QY 1 TNELQMDDKYSKSGIACFLKEDDSYDNDDEESMNSPCWQVQLRQLVRLKMLRTSEE 60
Db 39 TNELQMDDKYSKSGIACFLKEDDSYDNDDEESMNSPCWQVQLRQLVRLKMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYD 180
Db 159 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYD 218

QY 181 PILLMKSARNSCWSDAEYGLYSYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNSCWSDAEYGLYSYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
Db 279 LVG 281

RESULT 30
AAO29543
ID AAO29543 standard; protein; 281 AA.
XX

PS Claim 1; Col 45-48; 40pp; English.

XX The invention relates to an antibody that specifically binds: (a) the

CC human tumor necrosis factor (TNF) related apoptosis inducing ligand

CC (TRAIL) protein appearing as AB08558; (b) a soluble human TRAIL

CC polypeptide; (c) a polypeptide comprising amino acids 124-276 of

CC AB08558, or (d) a fragment of the TRAIL protein. Also included is an

CC antigen-binding fragment of the antibody (a monoclonal antibody), a

CC hybridoma cell line that produces the antibody. The antibody is used in

CC assays to detect the presence of TRAIL polypeptides, either in vitro or

CC in vivo, purifying TRAIL by affinity chromatography, blocking binding of

CC TRAIL to target cells and thus inhibiting a biological activity of TRAIL.

CC The antibody is useful for treating disorders mediated or exacerbated by

CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic

CC thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)

CC (even though it can strike children as well) small blood vessel clotting

CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic

CC lupus erythematosus (SLE). The present sequence represents human TRAIL

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYNDPDEESMNSPCWQVKQLRQLVKMLRTSEE 60

Db 39 TNELKQMDKYSGKGIACFLKEDDSYNDPDEESMNSPCWQVKQLRQLVKMLRTSEE 98

Qy 61 TISTVQEQKQNISPLVREGRQVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEQKQNISPLVREGRQVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVYIYKTSYPD 180

Db 159 SGHFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVYIYKTSYPD 218

Qy 181 PILLMKARNSCWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 219 PILLMKARNSCWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243

Db 279 LVG 281

RESULT 32

ABR42313

ID ABR42313 standard; protein; 281 AA.

XX

AC ABR42313;

XX

DT 11-AUG-2003 (first entry)

XX

DE Human TRAIL protein.

XX

XX Human; TRAIL; tumour necrosis factor; ligand; cytostatic;

KW immunomodulator; osteopathic.

XX

OS Homo sapiens.

XX

PN WO20003040307-A2.

XX

PD 15-MAY-2003.

XX

XX 25-JUL-2002; 2002WO-US023782.

PF

XX

PR 27-JUL-2001; 2001US-0307838P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

PA

XX Hilbert DE, Rosen CA;

PI

XX

DR WPI: 2003-430659/40.

DR N-PSDB; ACC57899.

XX

PT New heteromultimeric complex having a first polypeptide member of the

CC tumor necrosis factor (TNF) ligand family, and a second different member

CC of TNF ligand family, useful for treating cancer, osteoporosis or an

PT autoimmune disease.

XX

XX Disclosure; Page 364-365; 388pp; English.

PS

XX The present sequence is the protein sequence of human TRAIL polypeptide.

CC The invention relates to compositions comprising heterotrimeric complexes

CC of tumour necrosis factor (TNF) ligand family members, and their use in

CC the detection, prevention and treatment of disease. In one embodiment,

CC the heterotrimeric complex comprises full-length or extracellular

CC portions of TRAIL and full-length or extracellular portions of other TNF

CC ligand family members, preferably RANKL. The heterotrimeric complexes of

CC the invention are useful for treating an autoimmune disease, cancer or

CC osteoporosis, and particularly for inhibiting cancer cell proliferation,

CC increasing B cell proliferation, or inducing apoptosis of T cells. A

CC claimed method of inducing apoptosis of T cells comprises administering a

CC heterotrimeric complex consisting of FasL and LIGHT, TNF-alpha,

CC lymphotixin-beta or TRAIL. A claimed method of inhibiting cancer cell

CC proliferation involves administering a heterotrimeric complex consisting

CC of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis

CC comprises administering an antibody against a complex comprising RANKL

CC and TRAIL

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYNDPDEESMNSPCWQVKQLRQLVKMLRTSEE 60

Db 39 TNELKQMDKYSGKGIACFLKEDDSYNDPDEESMNSPCWQVKQLRQLVKMLRTSEE 98

Qy 61 TISTVQEQKQNISPLVREGRQVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEQKQNISPLVREGRQVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVYIYKTSYPD 180

Db 159 SGHFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVYIYKTSYPD 218

Qy 181 PILLMKARNSCWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 219 PILLMKARNSCWCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243

Db 279 LVG 281

RESULT 33

ABG71905

ID ABG71905 standard; protein; 281 AA.

XX

AC ABG71905;

XX

DT 20-JAN-2003 (first entry)

XX

DE Human TRAIL receptor-associated protein.

XX

XX Human; TRAIL receptor; tumour necrosis factor; TNF;

KW light chain variable region TNF-related apoptosis-inducing ligand;

KW antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7;

KW TR10; apoptosis; hyperproliferative disorder; hybridoma cell line;

KW Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease;

KW AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; autoimmune disorder;

KW multiple sclerosis; Behcet's disease; lupus erythematosus;

KW	inflammatory disease; rheumatoid arthritis; psoriasis; wound healing;	Db	39	TNELKQMDKYSGIACFLKEDDSYWDPNDBESMNSPCWQVKWLRLVRLKMLRTSBE	98
KW	cardiovascular disorder; angiogenesis; immune response;	Qy	61	TISTVOEKQONISPLVRERGPORVAHIITGTRSNLTSSPNSKNEKALGRKINSWESSR	120
XX	chemotherapeutic agent.	Db	99	TISTVOEKQONISPLVRERGPORVAHIITGTRSNLTSSPNSKNEKALGRKINSWESSR	158
OS	Homo sapiens.	Qy	121	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDP	180
PN	WO200279377-A2.	Db	159	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDP	218
PD	10-OCT-2002.	Qy	181	PILLMSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF	240
XX	07-NOV-2001; 2001WO-US042996.	Db	219	PILLMSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF	278
XX	08-NOV-2000; 2000US-0246612P.	Qy	241	LVG 243	
PR	16-NOV-2000; 2000US-0248847P.	Db	279	LVG 281	
PR	27-NOV-2000; 2000US-0252904P.				
PR	04-JUN-2001; 2001US-0295018P.				
PR	09-OCT-2001; 2001US-0327359P.				
XX	(HUMA-) HUMAN GENOME SCI INC.				
PA	Salcedo T, Roschke V, Ruben SM, Rosen CA;				
PI	WPI; 2003-040669/03.				
DR	Novel antibody for treating, or preventing disease or disorder, comprises				
PT	amino acid sequence having identity to other amino acid sequence of				
PT	either variable heavy/light chain-complementarity determining regions.				
XX	Disclosure; Page 366; 375pp; English.				
PS	The invention relates to an isolated antibody comprising a first amino				
XX	acid sequence having 95 % identity to a second amino acid sequence of				
CC	either variable heavy chain or light chain-complementarity determining				
CC	regions (VHCDRI)/VHCDRI, VHCDRI/VHCDRI or VHCDRI/VHCDRI appearing as				
CC	ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF				
CC	(tumour necrosis factor)-related apoptosis-inducing ligand receptor, also				
CC	known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that				
CC	produces the antibody, an antibody that binds the same epitope on a TR4				
CC	polypeptide as the antibody detailed above, detecting expression of a				
CC	TR4 polypeptide (or detecting, diagnosing, prognosing or monitoring				
CC	cancers, and other hyperproliferative disorders) using the antibodies, a				
CC	hybridoma cell line selected from the hybridoma cell lines contained in				
CC	ATCC Deposit No. PTA-3149, PTA-2687, PTA-3369, PTA-2730, PTA-2729, PTA-				
CC	2728, PTA-3368, and PTA-2731 and the antibodies expressed by these				
CC	hybridoma cell lines. The antibodies of the invention are useful for				
CC	diagnosing or treating a disease or disorder associated with increased or				
CC	decreased apoptosis, e.g. cancer (such as colon, breast, uterine,				
CC	pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versus-				
CC	host disease (GVHD), infectious disease, acquired immunodeficiency				
CC	syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's				
CC	disease, Parkinson's disease), autoimmune disorders like multiple				
CC	sclerosis, Behcet's disease, lupus erythematosus, inflammatory diseases				
CC	such as rheumatoid arthritis, and psoriasis, cardiovascular disorders, in				
CC	promoting angiogenesis, wound healing, and in regulating immune responses.				
CC	Many other diseases and disorders are listed in the specification. The				
CC	antibody is administered in combination with a chemotherapeutic agent				
CC	selected from irinotecan, paclitaxel (TAXOL (RTM), and gemcitabine. The				
CC	antibody is useful as a diagnostic tool to monitor the expression of				
CC	TRAIL receptor expression on cells, to detect, purify, and target the				
CC	polypeptides, and in immunoassays for qualitatively and quantitatively				
CC	measuring levels of TRAIL receptor polypeptides. The present sequence is				
CC	a human TRAIL receptor associated protein. Note: The present sequence is				
CC	included in the sequence listing but is not referred to anywhere else in				
CC	the specification				
XX	Sequence 281 AA;				
SQ	Query Match 100.0%; Score 1287; DB 6; Length 281;				
	Best Local Similarity 100.0%; Pred. No. 2.3e-117;				
	Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 TNELKQMDKYSGIACFLKEDDSYWDPNDBESMNSPCWQVKWLRLVRLKMLRTSBE 60				

is useful for detecting, diagnosing, prognosing, treating, preventing or ameliorating a disease or disorder associated with aberrant APRIL or APRIL receptor expression or aberrant function of APRIL or APRIL receptor. The disease or disorders includes autoimmune and inflammatory disorders such as antineutrophilic cytoplasmic autoantibody disease, asthma, allergic encephalomyelitis, myocarditis, hemolytic anemia, dermatitis, uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune system, particularly B cell cancers, immune disorders such as myasthenia gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease, infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and proliferative disorders (e.g. leukemia). The present sequence represents the tumour necrosis factor TRAIL

XX SQ Sequence 281 AA;
Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYDNDDESNMSPCWQVKQLRQLVRKMLRTSSE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYDNDDESNMSPCWQVKQLRQLVRKMLRTSSE 98
QY 61 TISTVQEQQNISPLVRERGPQVAHAITGTRGSNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEQQNISPLVRERGPQVAHAITGTRGSNTLSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQYTFPQSEIKENTKDKQVQYIYKTSYPD 180
DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQYTFPQSEIKENTKDKQVQYIYKTSYPD 218
QY 181 PILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 35
ID AAE36258 standard; protein; 281 AA.
AC AAE36258;
XX 26-JUN-2003 (first entry)
DT Human TR4 ligand, TRAIL protein.
DE
KW TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration; hyperproliferative disorder; neurodegenerative disorder; immune disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis; rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma; biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder; glomerulonephritis; immune deficiency syndrome; myasthenia gravis; polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock; infectious disease; acquired immunodeficiency syndrome; viral infection; AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia; ischaemic injury; myocardial infarction; reperfusion injury; cachexia; anorexia; stroke; cardiovascular disorder; peripheral artery disease; limb ischaemia; arrhythmia; congestive heart failure; neovascularisation; ocular disorder; wound healing; angiogenesis; transplantation; human.
OS Homo sapiens.
XX WO200297033-A2.
FN
XX
PD 05-DEC-2002.
XX
PF 07-MAY-2002; 2002WO-US014268.
XX

PR 25-MAY-2001; 2001US-0293473P.
PR 04-JUN-2001; 2001US-0294981P.
PR 02-AUG-2001; 2001US-0309176P.
PR 21-SEP-2001; 2001US-0323807P.
PR 09-OCT-2001; 2001US-0323807P.
PR 07-NOV-2001; 2001US-0331044P.
PR 14-NOV-2001; 2001US-0331310P.
PR 20-DEC-2001; 2001US-0341237P.
PR 05-APR-2002; 2002US-0369860P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;
PI
XX MPI; 2003-140454/13.
XX

Novel antibody useful for treating cancers and other hyperproliferative disorders, immunospecifically binds to TRAIL receptor and comprises variable heavy or light chain complementarity determining regions.
Disclosure; Page 300-301; 301pp; English.
The present invention relates to novel antibodies that immunospecifically bind to TRAIL receptor (TR4). Sequences of the invention are useful for treating, preventing or ameliorating cancer (e.g. colon, breast, uterine, pancreatic, lung, gastrointestinal or central nervous system cancer e.g. medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in human. They are useful for detecting expression of TR4 polypeptide and proliferative disorders. Antibodies of the invention are useful for treating, preventing or ameliorating neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, cerebellar degeneration and Huntington's disease), immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis, Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, immune-related glomerulonephritis, myasthenia gravis, Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory disorders (e.g. asthma, allergic disorders and rheumatoid arthritis), infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS), herpes viral infections and other viral infections) and proliferative disorders. They are also useful for treating myelodysplastic syndromes (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke, myocardial infarction and reperfusion injury), septic shock, cachexia, anorexia and toxin-induced liver diseases (such as alcohol). They are also useful for treating cardiovascular disorders including peripheral artery diseases such as limb ischaemia, arrhythmia, congestive heart failure and cardiovascular tuberculosis, diseases or disorders associated with neovascularisation and ocular disorders, for wound healing, for promoting angiogenesis and as adjuvants to enhance immune responsiveness to specific antigen e.g. viral antigen. They are also useful in the preparation or recovery from surgery, trauma, radiation therapy and transplantation. The present sequence is human TR4 ligand, TRAIL protein used in the invention
SQ Sequence 281 AA;
Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYDNDDESNMSPCWQVKQLRQLVRKMLRTSSE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYDNDDESNMSPCWQVKQLRQLVRKMLRTSSE 98
QY 61 TISTVQEQQNISPLVRERGPQVAHAITGTRGSNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEQQNISPLVRERGPQVAHAITGTRGSNTLSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQYTFPQSEIKENTKDKQVQYIYKTSYPD 180
DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQYTFPQSEIKENTKDKQVQYIYKTSYPD 218
QY 181 PILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 219 PILLMKSARNCSWSDAEYGLYIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281
RESULT 36
ID AAO31151
XX AAO31151 standard; protein; 281 AA.
AC AAO31151;
DT 06-OCT-2003 (first entry)
XX Human TNF-related apoptosis-inducing ligand (TRAIL).
XX Human; protein coordinate data; heavy chain variable domain; VH; cancer;
KW complementarity determining region; CDR; light chain variable domain; VL;
KW TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
KW DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
KW glioblastoma; graft versus host disease; antibody therapy; neotropic;
KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
KW immunosuppressive; neuroprotective; antibody therapy; antibody.
XX Homo sapiens.
XX WO2003054216-A2.
XX 03-JUL-2003.
XX 19-DEC-2002; 2002WO-US040597.
XX 20-DEC-2001; 2001US-0341237P.
XX 05-APR-2002; 2002US-0369877P.
XX 04-JUN-2002; 2002US-0384828P.
XX 18-JUL-2002; 2002US-0396591P.
XX 15-AUG-2002; 2002US-0403370P.
XX 13-NOV-2002; 2002US-0425737P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
XX WPI; 2003-569250/53.
XX New antibody or its fragment, useful for treating, preventing or
PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
PT disease, AIDS.
XX Disclosure; Page 297-298; 301pp; English.
XX The invention relates to an isolated antibody or its fragments such as
CC VHCDR1 (heavy chain variable domain complementarity determining region),
CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment
CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
CC antibody or its fragment is useful for treating, preventing or
CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or
CC a neurodegenerative disorder. The invention is useful in antibody
CC therapy. The present sequence is human TRAIL
XX Sequence 281 AA;
SQ Query Match 100.0%; Score 1287; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWOLRQIVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWOLRQIVRKMLRTSEE 98
QY 61 TISTVQEKQKNISPLVREERGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQKNISPLVREERGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLNLHRLNGELVIHEKGFYIYSQYFFQBEIKENTKDKOMQVYIYKTSYPD 180
Db 159 SGHSFLNLHRLNGELVIHEKGFYIYSQYFFQBEIKENTKDKOMQVYIYKTSYPD 218
QY 181 PILLMKSARNCSWSDAEYGLYIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWSDAEYGLYIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281
RESULT 37
ID ABO25125 standard; protein; 281 AA.
XX ABO25125;
XX AC ABO25125;
XX DT 05-SEP-2003 (first entry)
XX DE Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.
XX KW Human; DNA methylation; cancer; colon cancer.
XX OS Homo sapiens.
XX PN US2003013099-A1.
XX PD 16-JAN-2003.
XX PF 07-MAR-2002; 2002US-00093766.
XX PR 19-MAR-2001; 2001US-0277380P.
XX (LASE/) LASEK A K W.
XX (JONE/) JONES D A.
XX (KARP/) KARP A R.
XX Lasek AKW, Jones DA, Karpf AR;
XX WPI; 2003-503249/47.
XX N-PSDB; ACD42246.
XX New combination comprising cDNAs that are expressed in a disorder or
PT process associated with DNA methylation, useful for diagnosing, staging,
PT treating or monitoring treatment of cancer, e.g. colon cancer.
XX Disclosure; Page 56-57; 66pp; English.
XX The invention relates to a combination comprising cDNAs which are
CC expressed in a disorder or process associated with DNA methylation. The
CC combination and cDNAs are useful for diagnosing, staging, treating or
CC monitoring treatment of cancer, e.g. colon cancer and for detecting
CC changes in expression of genes encoding proteins that are associated with
CC DNA methylation. The protein is useful for screening molecules or
CC compounds to identify at least one ligand that binds to the protein and
CC for producing an antibody. The present sequence represents the amino acid
CC sequence of a protein expressed in a disorder or process associated with
CC DNA methylation
XX Sequence 281 AA;
SQ

Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQVLRKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQVLRKMLRTSEE 98

QY 61 TISTVQEKQNIPLVREGRGQVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNIPLVREGRGQVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFSLNHLRNGELVHEKGFYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYDP 180
DB 159 SGHSFSLNHLRNGELVHEKGFYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYDP 218

QY 181 PILLKSGARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKSGARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 38
ADB61471
ID ADB61471 standard; protein; 281 AA.
XX AC ADB61471;
XX DT 04-DEC-2003 (first entry)
XX DE Native human Apo-2 ligand protein.
XX KW Apo-2 ligand; DR5 Apo2L complex; receptor contact region;
XX KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
XX KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
XX KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
XX KW native; human.
XX OS Homo sapiens.
XX PN WO2003029420-A2.
XX PD 10-APR-2003.
XX PF 01-OCT-2002; 2002WO-US031210.
XX PR 02-OCT-2001; 2001US-0326622P.
XX PA (GETH) GENENTECH INC.
XX PI Kelley RF, Lindstrom SH;
XX DR WPI; 2003-541400/51.
XX DR N-PSDB; ADB61470.
XX PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
XX PT cancer or an immune-related disease such as multiple sclerosis, comprises
XX PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX PS Claim 1; Fig 1; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at CC residue positions identified from x-ray crystal structure of the DR5-Apo2L complex. The polypeptide having the substitutions made at CC residue position(s) selected from 20 positions such as S96C, S101C, S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,

CC R170K, R170S, K179C, D234C, E249C, R255C, E264C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5-Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the native human Apo-2 ligand protein of
CC the invention.

SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQVLRKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQVLRKMLRTSEE 98

QY 61 TISTVQEKQNIPLVREGRGQVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNIPLVREGRGQVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFSLNHLRNGELVHEKGFYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYDP 180
DB 159 SGHSFSLNHLRNGELVHEKGFYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYDP 218

QY 181 PILLKSGARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKSGARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 39
ADC35202
ID ADC35202 standard; protein; 281 AA.

XX AC ADC35202;
XX DT 18-DEC-2003 (first entry)
XX DE Human TNF ligand family member #10.
XX KW human; tumor necrosis factor; TNF ligand; endokine alpha;
XX KW excessive bone resorption disorder; osteoporosis; Paget's disease;
XX KW arterial calcification.

XX OS Homo sapiens.
XX PN US2003100074-A1.
XX PD 29-MAY-2003.
XX PF 15-AUG-2002; 2002US-00218547.
XX PR 16-AUG-2001; 2001US-0312542P.
XX PR 30-OCT-2001; 2001US-0330761P.
XX PA (YUGG/) YU G.

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PA (NIJ/) NI J.
PA (ROSE/) ROSEN C A.
XX (NARD/) NARDELLI B.
PI Yu G, Ni J, Rosen CA, Nardelli B;
XX WPI; 2003-696072/66.
DR N-PSDB; ADC35201.
XX
XX New Endokine alpha gene useful for preparing a composition for treating a
PT disease associated with excessive or insufficient bone resorption e.g.,
PT osteoporosis, Paget's disease or arterial calcification.
XX
XX Disclosure; SEQ ID NO 20; 145pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
CC tumour necrosis factor family ligand. A composition comprising the
CC isolated antibody or its fragment is used for treating an individual in
CC need of decreased level of endokine alpha activity. The endokine alpha
CC polypeptide present in a heterotrimeric complex is used for treating an
CC individual having a disorder associated with excessive bone resorption,
CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
CC individual having a disorder associated with insufficient bone resorption
CC comprises administering an endokine alpha antagonist, which is the
CC antibody that binds specifically to endokine alpha polypeptide. The
CC present sequence represents the amino acid sequence of a tumour necrosis
CC factor family ligand.
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1287; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELQMDQKYSKSGIACFLKEDDSYWDPNDESNMSPCWQVKQLRQLVKRMILRTSEE 60
DB 39 TNELQMDQKYSKSGIACFLKEDDSYWDPNDESNMSPCWQVKQLRQLVKRMILRTSEE 98
QY 61 TISTVQEKQONISPLVRRGQPVAAHITCTGRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRRGQPVAAHITCTGRGNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLNLHLRNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 180
DB 159 SGHSFLNLHLRNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 218
QY 181 PILLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281
RESULT 40
ADD14080
ID ADD14080 standard; protein; 281 AA.
XX
XX AC ADD14080;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human src biomarker polypeptide SEQ ID NO:269.
XX
XX predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human.
XX
XX Homo sapiens.
XX
XX WO2003062395-A2.
XX

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PD 31-JUL-2003.
XX
XX 17-JAN-2003; 2003WO-US001981.
XX PF
XX 18-JAN-2002; 2002US-0350061P.
XX PR
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PA
XX Huang F, Fairchild CR, Lee FY, Shaw P;
XX PI
XX WPI; 2003-636735/60.
XX DR
XX N-PSDB; ADD14676.
XX
XX New polynucleotides and polypeptides for predicting the activity of
PT compounds that interact with protein tyrosine kinases and/or protein
PT tyrosine kinase pathways.
XX
XX Claim 10; SEQ ID NO 269; 139pp; English.
XX
XX The present invention describes a predictor set comprising a plurality of
CC polynucleotides or polypeptides whose expression pattern is predictive of
CC the response of cells to treatment with a compound that modulates protein
CC tyrosine kinase activity or members of the protein tyrosine kinase
CC pathway. Also described: (1) predicting whether a compound is capable of
CC modulating the activity of cells, comprising obtaining a sample of cells,
CC determining whether the cells express a plurality of markers, and
CC correlating the expression of the markers to the compound's ability to
CC modulate the activity of the cells; (2) a plurality of cell lines for
CC identifying polynucleotides and polypeptides whose expression levels
CC correlate with compound sensitivity or resistance of cells associated
CC with a disease state; and (3) identifying polynucleotides and
CC polypeptides that predict compound sensitivity or resistance of cells
CC associated with a disease state, comprising subjecting the plurality of
CC cell lines to one or more compounds, analysing the expression pattern of
CC a microarray of polynucleotides or polypeptides, and selecting or
CC polynucleotides or polypeptides that predict the sensitivity or
CC resistance of cells associated with a disease state by using the
CC expression pattern of the microarray. The polynucleotides and
CC polypeptides have cytostatic activities, and can be used in gene therapy.
CC The polynucleotides and polypeptides are useful in predicting the
CC activity of compounds that interact with protein tyrosine kinases and/or
CC protein tyrosine kinase pathways. These may be used in determining drug
CC sensitivity in patients to allow the development of individualized
CC genetic profiles which aid in treating diseases and disorders (e.g.
CC cancer) based on patient response at a molecular level. The present
CC sequence is used in the exemplification of the present invention.
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1287; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELQMDQKYSKSGIACFLKEDDSYWDPNDESNMSPCWQVKQLRQLVKRMILRTSEE 60
DB 39 TNELQMDQKYSKSGIACFLKEDDSYWDPNDESNMSPCWQVKQLRQLVKRMILRTSEE 98
QY 61 TISTVQEKQONISPLVRRGQPVAAHITCTGRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRRGQPVAAHITCTGRGNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLNLHLRNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 180
DB 159 SGHSFLNLHLRNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYD 218
QY 181 PILLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

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QY	121	SGHSFLSNLHRLNGELVTHKGFYIYISQTYFRQEBIKENTKNDKQWQVIYKYTSYD	218
Db	159	SGHSFLSNLHRLNGELVTHKGFYIYISQTYFRQEBIKENTKNDKQWQVIYKYTSYD	219
QY	181	PILLKMSARNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240
Db	219	PILLKMSARNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278
QY	241	LVG 243	
Db	279	LVG 281	
RESULT 42			
ID	ADE76953		
XX	AC	ADE76953 standard; protein; 281 AA.	
XX	AC	ADE76953;	
XX	DT		
XX	DT	29-JAN-2004 (first entry)	
XX	DE	Human protein expressed in a liver disorder #32.	
XX	KW	human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;	
XX	KW	tumour; liver; inflammatory disorder; immune response disorder;	
XX	KW	high-throughput screening; differential gene expression; gene therapy.	
XX	OS	Homo sapiens.	
XX	XX	US2003109871-A1.	
XX	XX	12-JUN-2003.	
XX	XX	30-JUL-2001; 2001US-00919039.	
XX	XX	28-JUL-2000; 2000US-0222113P.	
XX	XX	(KASE/) KASER M R.	
XX	PI	Kaser MR;	
XX	XX	WPI: 2004-031227/03.	
XX	DR	N-PSDB; ADE76952.	
XX	XX	Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver disorders.	
XX	PS	Claim 1; SEQ ID NO 118; 41pp; English.	
XX	CC	The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a liver disorder.	
XX	XX	Sequence 281 AA;	

Query Match 100.0%; Score 1287; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TNELKQMDKYSGSGIACFLKEDDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEE	60
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Qy	61	TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120
Db	99	TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	158
Qy	121	SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQBEIKENTKDKQWQYIYKYSYD	180
Db	159	SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQBEIKENTKDKQWQYIYKYSYD	218
Qy	181	PILLMKSARNCSWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240
Db	219	PILLMKSARNCSWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278
Qy	241	LVG 243	
Db	279	LVG 281	

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Job time : 64 secs

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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:53:00 ; Search time 22 Seconds
(without alignments)
570.232 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	279	US-09-072-993C-3	Sequence 3, Appli
2	1287	100.0	281	US-08-670-354-2	Sequence 2, Appli
3	1287	100.0	281	US-08-584-031-1	Sequence 1, Appli
4	1287	100.0	281	US-08-780-496-1	Sequence 1, Appli
5	1287	100.0	281	US-08-883-086-10	Sequence 10, Appli
6	1287	100.0	281	US-09-320-424-2	Sequence 2, Appli
7	1287	100.0	281	US-09-333-593A-6	Sequence 6, Appli
8	1287	100.0	281	US-09-157-864-11	Sequence 11, Appli
9	1287	100.0	281	US-09-825-563-2	Sequence 2, Appli
10	1287	100.0	281	US-10-039-785-66	Sequence 66, Appli
11	1287	100.0	281	PCT-US96-10895-2	Sequence 2, Appli
12	988	76.8	253	US-09-320-424-11	Sequence 11, Appli
13	988	76.8	253	US-09-825-563-11	Sequence 11, Appli
14	988	76.8	256	US-09-320-424-13	Sequence 13, Appli
15	988	76.8	256	US-09-825-563-13	Sequence 13, Appli
16	930	72.3	177	US-09-105-343A-7	Sequence 7, Appli
17	863	67.1	291	US-08-670-354-6	Sequence 6, Appli
18	863	67.1	291	US-09-320-424-6	Sequence 6, Appli
19	863	67.1	291	US-09-825-563-6	Sequence 6, Appli
20	863	67.1	291	PCT-US96-10895-6	Sequence 6, Appli
21	850	66.0	161	US-09-565-423-7	Sequence 7, Appli
22	654	50.8	183	US-09-105-343A-8	Sequence 8, Appli
23	446	34.7	85	US-09-632-287A-12	Sequence 12, Appli
24	291	22.6	101	US-08-670-354-4	Sequence 4, Appli
25	291	22.6	101	US-09-320-424-4	Sequence 4, Appli
26	291	22.6	101	US-09-825-563-4	Sequence 4, Appli
27	291	22.6	101	PCT-US96-10895-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3

Query Match 100.0%; Score 1287; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCQVKQKQLRQVRKMLRTSEE 60
Db 37 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCQVKQKQLRQVRKMLRTSEE 96
QY 61 TISTVQEKQONISPLVRRGPGORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 97 TISTVQEKQONISPLVRRGPGORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156
QY 121 SGHSFLSNLHNLNGELVTHKGFYIYSQTYFRFOEEKENTKDKQWQVYIKYTSYD 180
Db 157 SGHSFLSNLHNLNGELVTHKGFYIYSQTYFRFOEEKENTKDKQWQVYIKYTSYD 216
QY 181 PILLMKSAFNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAF 240
Db 217 PILLMKSAFNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAF 276
QY 241 LVG 243
Db 277 LVG 279

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RESULT 2
US-08-670-354-2
; Sequence 1, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 100.0%; Score 1287; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEE 98
QY 61 TISTVQEKQNISPLVREGRQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNISPLVREGRQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIKENTKNDKQWQVYIKYTSYD 180
DB 159 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIKENTKNDKQWQVYIKYTSYD 218
QY 181 PILLMKSGNSCKSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSGNSCKSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 3
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEE 98
QY 61 TISTVQEKQNISPLVREGRQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNISPLVREGRQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIKENTKNDKQWQVYIKYTSYD 180
DB 159 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIKENTKNDKQWQVYIKYTSYD 218
QY 181 PILLMKSGNSCKSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSGNSCKSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 4
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-496-1

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDP 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDP 218
QY 181 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 5
US-08-883-086-10
Sequence 10, Application US/08883086
Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foremski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDP 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDP 218
QY 181 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 6
US-09-320-424-2
Sequence 2, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 281
TYPE: PRT
ORGANISM: human
US-09-320-424-2

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158


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/ FILE REFERENCE: 2835-E
/ CURRENT APPLICATION NUMBER: US/09/825,563
/ CURRENT FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: 09/320,424
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: 09/190,046
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: 09/048,641
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 08/670,354
/ PRIOR FILING DATE: 1996-06-25
/ PRIOR APPLICATION NUMBER: 08/548,368
/ PRIOR FILING DATE: 1995-11-01
/ PRIOR APPLICATION NUMBER: 08/496,632
/ PRIOR FILING DATE: 1995-06-29
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 281
/ TYPE: PRT
/ ORGANISM: human
US-09-825-563-2

Query Match      100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCWQVQWLQRLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCWQVQWLQRLVRKMLRTSEE 98
QY 61 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQWQVYIKYTSYDP 180
Db 159 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQWQVYIKYTSYDP 218
QY 181 PILLKMSARNSCWKDAEYGLIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNSCWKDAEYGLIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 10
PCT-US96-10895-66
/ Sequence 66, Application US/10039785
/ Patent No. 6538938
/ GENERAL INFORMATION:
/ APPLICANT: Salcedo et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: PF550
/ CURRENT APPLICATION NUMBER: US/10/039,785
/ CURRENT FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 60/369,860
/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/341,237
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/331,310
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/331,044
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: 60/327,364
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/323,807
/ PRIOR FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/309,176
/ PRIOR FILING DATE: 2001-08-02

US-10-039-785-66
/ Sequence 66, Application PC/TUS9610895
/ GENERAL INFORMATION:
/ APPLICANT: Immunex Corporation.
/ TITLE OF INVENTION: Cytokine That Induces Apoptosis
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Apple 7.5.2
/ SOFTWARE: Microsoft Word, Version 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/10895
/ FILING DATE: 25-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/496,632
/ FILING DATE: 29-JUN-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/548,368
/ FILING DATE: 01-NOV-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Anderson, Kathryn A.
/ REGISTRATION NUMBER: 32,172
/ REFERENCE/DOCKET NUMBER: 2835-WO
/ TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 100.0%; Score 1287; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVRKMLRTSBE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVRKMLRTSBE 98
QY 61 TISVQEKQNIISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 120
DB 99 TISTVQEKQNIISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 158
QY 121 SGHSFSLNHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYD 180
DB 159 SGHSFSLNHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYD 218
QY 181 PILLMKARSNSCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 240
DB 219 PILLMKARSNSCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; EARLIER FILING DATE: 1999-05-26
; EARLIER FILING DATE: 1998-11-10
; EARLIER FILING DATE: 1998-11-10
; EARLIER FILING DATE: 1998-03-26
; EARLIER FILING DATE: 1996-06-25
; EARLIER FILING DATE: 1995-11-01
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match 76.8%; Score 988; DB 3; Length 253;
Best Local Similarity 78.9%; Pred. No. 2e-94;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVK---WQLRQLVRKMLRT 57
DB 29 SDRMKQIEDKI-----EELSKIYHIENIARIKKLIGERTST 67

QY 58 SEETISTVQEKQNIISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 117
DB 68 SEETISTVQEKQNIISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 127
QY 118 SSRSCHSFLSNLHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQVQYIYKTS 177
DB 128 SSRSCHSFLSNLHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQVQYIYKTS 187
QY 178 YPDPILLMKARSNSCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 237
DB 188 YPDPILLMKARSNSCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 247
QY 238 GAFLVG 243
DB 248 GAFLVG 253

RESULT 13
US-09-825-563-11
; Sequence 11, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-11

Query Match 76.8%; Score 988; DB 4; Length 253;
Best Local Similarity 78.9%; Pred. No. 2e-94;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVK---WQLRQLVRKMLRT 57
DB 29 SDRMKQIEDKI-----EELSKIYHIENIARIKKLIGERTST 67
QY 58 SEETISTVQEKQNIISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 117
DB 68 SEETISTVQEKQNIISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 127
QY 118 SSRSCHSFLSNLHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQVQYIYKTS 177
DB 128 SSRSCHSFLSNLHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQVQYIYKTS 187
QY 178 YPDPILLMKARSNSCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 237
DB 188 YPDPILLMKARSNSCKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 247
QY 238 GAFLVG 243
DB 248 GAFLVG 253


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RESULT 14
US-09-320-424-13
; Sequence 13, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; EARLIER FILING DATE: 1999-05-26
; EARLIER FILING DATE: 1998-11-10
; EARLIER FILING DATE: 1998-03-26
; EARLIER FILING DATE: 1998-03-26
; EARLIER FILING DATE: 1996-06-25
; EARLIER FILING DATE: 1996-06-25
; EARLIER FILING DATE: 1995-11-01
; EARLIER FILING DATE: 1995-11-01
; EARLIER FILING DATE: 1995-06-29
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
; US-09-320-424-13

Query Match      76.8%; Score 988; DB 3; Length 256;
Best Local Similarity 78.9%; Pred. No. 2e-94;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVK---WQLRQLVRKMLRT 57
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Db 32 SDRMKQIEDKI-----BEILSKIYHIENEIARIKKGIGERTST 70

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; Sequence 13, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-R
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
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; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
; US-09-825-563-13

Query Match      76.8%; Score 988; DB 4; Length 256;
Best Local Similarity 78.9%; Pred. No. 2e-94;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

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Qy 178 YPDPIILMKSGARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 237
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Qy 238 GAFLVG 243
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Db 251 GAFLVG 256

Search completed: June 3, 2004, 08:56:54
Job time : 23 secs
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